

SEQUENCE LISTING

<110> Hibom, Gert
Menke, Annette

<120> Influenza Viruses with Enhanced Transcriptional and Replicative Capacities

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 aaccattga atg gtc aat ccg act tta ctg ttc ttg aaa gtt cct 229
 Met Asp Val Asn Pro Thr Leu Leu Phe Leu Lys Val Pro
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 Ala Gln Asn Ala Ile Ser Thr Thr Phe Pro Tyr Thr Gly Asp Pro Pro
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tac agg cat gga aca ggg aca gga tac acc atg gac aca gtc aac agg 325
 Tyr Ser His Gly Thr Gly Thr Gly Tyr Thr Met Asp Thr Val Asn Arg
 30 35 40 45

aca cat caa tat tcg gaa aag ggg aaa tgg aca aca aac act gag act 373
 Thr His Gln Tyr Ser Glu Lys Gly Lys Trp Thr Thr Asn Thr Glu Thr
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 Gly Ala Pro Gln Leu Asn Pro Ile Asp Gly Pro Leu Pro Glu Asp Asn
 65 70 75

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Glu Pro Ser Gly Tyr Ala Gln Thr Asp Cys Val Leu Glu Ala Met Ala	
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ttc ctt gaa gaa tcc cat cca gga atc ttt gaa aac tcg tgt ctt gag	517
Phe Leu Glu Glu Ser His Pro Gly Ile Phe Glu Asn Ser Cys Leu Glu	
95 100 105	
acg atg gaa gtt gtt caa caa aca aga gtg gac aaa ctg acc caa ggc	565
Thr Met Glu Val Val Gln Gln Thr Arg Val Asp Lys Leu Thr Gln Gly	
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Arg Gln Thr Tyr Asp Trp Thr Leu Asn Arg Asn Gln Pro Ala Ala Thr	
130 135 140	
gca tta gca aac act ata gag gtc ttt aga tcg aat ggt cta aca gct	661
Ala Leu Ala Asn Thr Ile Glu Val Phe Arg Ser Asn Gly Leu Thr Ala	
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Asn Glu Ser Gly Arg Leu Ile Asp Phe Leu Lys Asp Val Met Glu Ser	
160 165 170	
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Met Asp Lys Glu Glu Met Glu Ile Thr Thr His Phe Gln Arg Lys Arg	
175 180 185	
aga gta aga gac aac atg acc aag aaa atg gtc aca caa aga aca ata	805
Arg Val Arg Asp Asn Met Thr Lys Lys Met Val Thr Gln Arg Thr Ile	
190 195 200 205	
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Gly Lys Lys Gln Arg Leu Asn Lys Arg Ser Tyr Leu Ile Arg Ala	
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Leu Thr Leu Asn Thr Met Thr Lys Asp Ala Glu Arg Gly Lys Leu Lys	
225 230 235	
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Arg Arg Ala Ile Ala Thr Pro Gly Met Gln Ile Arg Gly Phe Val Tyr	
240 245 250	
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Phe Val Glu Thr Leu Ala Arg Ser Ile Cys Glu Lys Leu Glu Gln Ser	
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Val Arg Lys Met Met Thr Asn Ser Gln Asp Thr Glu Leu Ser Phe Thr	
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Asn Glu Pro Thr Arg Lys Lys Ile Glu Lys Ile Arg Pro Leu Ile Ile	
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Asp Gly Thr Ala Ser Leu Ser Pro Gly Met Met Met Gly Met Phe Asn	
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Met Leu Ser Thr Val Leu Gly Val Ser Ile Leu Asn Leu Gly Gln Lys	
415 420 425	
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430 435 440 445	
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Pro Ser Phe Gly Val Ser Gly Ile Asn Glu Ser Ala Asp Met Ser Ile	
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Gly Val Thr Val Ile Lys Asn Asn Met Ile Asn Asn Asp Leu Gly Pro	
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Thr Tyr Arg Cys His Arg Gly Asp Thr Gln Ile Gln Thr Arg Arg Ser	
560 565 570	
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Phe Glu Leu Lys Lys Leu Trp Glu Gln Thr Arg Ser Lys Ala Gly Leu	
575 580 585	
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750 755

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Glu	Ser	His	Pro	Gly	Ile	Phe	Glu	Asn	Ser	Cys	Leu	Glu	Thr	Met	Glu
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Val	Val	Gln	Gln	Thr	Arg	Val	Asp	Lys	Leu	Thr	Gln	Gly	Arg	Gln	Thr
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Gly	Arg	Leu	Ile	Asp	Phe	Leu	Lys	Asp	Val	Met	Glu	Ser	Met	Asp	Lys
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Glu	Glu	Met	Glu	Ile	Thr	Thr	His	Phe	Gln	Arg	Lys	Arg	Arg	Val	Arg
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Asp	Asn	Met	Thr	Lys	Lys	Met	Val	Thr	Gln	Arg	Thr	Ile	Gly	Lys	Lys
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Lys	Gln	Arg	Leu	Asn	Lys	Arg	Ser	Tyr	Leu	Ile	Arg	Ala	Leu	Thr	Leu
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Asn	Thr	Met	Thr	Lys	Asp	Ala	Glu	Arg	Gly	Lys	Leu	Lys	Arg	Arg	Ala
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Ile	Ala	Thr	Pro	Gly	Met	Gln	Ile	Arg	Gly	Phe	Val	Tyr	Phe	Val	Glu
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 Lys Gly Tyr Met Phe Glu Ser Lys Ser Met Lys Leu Arg Thr Gln Ile
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 Thr Arg Lys Lys Ile Glu Lys Ile Arg Pro Leu Ile Ile Asp Gly Thr
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 Tyr Asp Ala Val Ala Thr Thr His Ser Trp Ile Pro Lys Arg Asn Arg
 660 665 670
 Ser Ile Leu Asn Thr Ser Gln Arg Gly Ile Leu Glu Asp Glu Gln Met
 675 680 685

Tyr Gln Lys Cys Cys Asn Leu Phe Glu Lys Phe Phe Pro Ser Ser Ser
 690 695 700
 Tyr Arg Arg Pro Val Gly Ile Ser Ser Met Val Glu Ala Met Val Ser
 705 710 715 720
 Arg Ala Arg Ile Asp Ala Arg Ile Asp Phe Glu Ser Gly Arg Ile Lys
 725 730 735
 Lys Glu Glu Phe Ala Glu Ile Met Lys Ile Cys Ser Thr Ile Glu Glu
 740 745 750
 Leu Arg Arg Gln Lys
 755

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 <211> 5169
 <212> DNA
 <213> Artificial Sequence

<220>
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 acaaagtgtc gcccggagta ctggtcgacc tccgaagttg ggggggagcgc aaagcaggca 180
 aaccatggatg gatgtc aatccg acttta cttttc ttaaaa gtgtccaa 229
 Met Asp Val Asn Pro Thr Leu Leu Phe Leu Lys Val Pro
 1 5 10

gca caaaatgtata agcaca actttc ccttat actggagccctccct 277
 Ala Gln Asn Ala Ile Ser Thr Thr Phe Pro Tyr Thr Gly Asp Pro Pro
 15 20 25

tac agc cat ggg aca gga aca gga tac acc atg gat act gtc aac agg 325
 Tyr Ser His Gly Thr Gly Thr Gly Tyr Thr Met Asp Thr Val Asn Arg
 30 35 40 45

aca cat cag tac tca gaa agg gga aga tgg aca aca aac acc gaa act 373
 Thr His Gln Tyr Ser Glu Arg Gly Arg Trp Thr Thr Asn Thr Glu Thr
 50 55 60

gga gca ccg caa ctc aac ccg att gat ggg cca ctg cca gaa gac aat 421
 Gly Ala Pro Gln Leu Asn Pro Ile Asp Gly Pro Leu Pro Glu Asp Asn
 65 70 75

gaa cca agt ggt tat gcc caa aca gat tgt gta ttg gaa gca atg gcc 469
 Glu Pro Ser Gly Tyr Ala Gln Thr Asp Cys Val Leu Glu Ala Met Ala
 80 85 90

ttc ctt gag gaa tcc cat cct ggt atc ttt gag acc tcg tgt ctt gaa 517
 Phe Leu Glu Glu Ser His Pro Gly Ile Phe Glu Thr Ser Cys Leu Glu
 95 100 105

acg atg gag gtt gtt cag caa aca cga gtg gac aag ctg aca caa ggc 565
 Thr Met Glu Val Val Gln Gln Thr Arg Val Asp Lys Leu Thr Gln Gly
 110 115 120 125

cga cag acc tat gac tgg act cta aat agg aac cag cct gct gca aca	613
Arg Gln Thr Tyr Asp Trp Thr Leu Asn Arg Asn Gln Pro Ala Ala Thr	
130 135 140	
gca ttg gcc aac aca ata gaa gta ttc aga tca aat ggc ctc acg gcc	661
Ala Leu Ala Asn Thr Ile Glu Val Phe Arg Ser Asn Gly Leu Thr Ala	
145 150 155	
aat gaa tct gga agg ctc ata gac ttc ctt aag gat gta atg gag tca	709
Asn Glu Ser Gly Arg Leu Ile Asp Phe Leu Lys Asp Val Met Glu Ser	
160 165 170	
atg aac aaa gaa gaa atg gag atc aca act cat ttt cag aga aag aga	757
Met Asn Lys Glu Glu Met Glu Ile Thr Thr His Phe Gln Arg Lys Arg	
175 180 185	
cga gtg aga gac aat atg act aag aaa atg gtg aca cag aga aca ata	805
Arg Val Arg Asp Asn Met Thr Lys Lys Met Val Thr Gln Arg Thr Ile	
190 195 200 205	
ggg aaa agg aag cag aga ttg aac aaa agg agt tat cta att agg gca	853
Gly Lys Arg Lys Gln Arg Leu Asn Lys Arg Ser Tyr Leu Ile Arg Ala	
210 215 220	
tta acc ctg aac aca atg acc aaa gat gct gag aga ggg aag cta aaa	901
Leu Thr Leu Asn Thr Met Thr Lys Asp Ala Glu Arg Gly Lys Leu Lys	
225 230 235	
cgg aga gca att gca acc cca ggg atg caa ata agg ggg ttt gta tac	949
Arg Arg Ala Ile Ala Thr Pro Gly Met Gln Ile Arg Gly Phe Val Tyr	
240 245 250	
ttt gtt gag aca cta gca agg agt ata tgt gag aaa ctt gaa caa tca	997
Phe Val Glu Thr Leu Ala Arg Ser Ile Cys Glu Lys Leu Glu Gln Ser	
255 260 265	
gga ttg cca gtt gga ggc aat gag aag aaa gca aag ttg gca aat gtt	1045
Gly Leu Pro Val Gly Gly Asn Glu Lys Lys Ala Lys Leu Ala Asn Val	
270 275 280 285	
gta agg aag atg atg acc aat tct cag gac act gaa att tct ttc acc	1093
Val Arg Lys Met Met Thr Asn Ser Gln Asp Thr Glu Ile Ser Phe Thr	
290 295 300	
atc act gga gat aac acc aaa tgg aac gaa aat cag aac cct cgg atg	1141
Ile Thr Gly Asp Asn Thr Lys Trp Asn Glu Asn Gln Asn Pro Arg Met	
305 310 315	
ttt ttg gcc atg atc aca tat ata acc aga aat cag ccc gaa tgg ttc	1189
Phe Leu Ala Met Ile Thr Tyr Ile Thr Arg Asn Gln Pro Glu Trp Phe	
320 325 330	
aga aat gtt cta agt att gct cca ata atg ttc tca aac aaa atg gcg	1237
Arg Asn Val Leu Ser Ile Ala Pro Ile Met Phe Ser Asn Lys Met Ala	
335 340 345	
aga ctg gga aag ggg tac atg ttt gag agc aag agt atg aaa att aga	1285
Arg Leu Gly Lys Gly Tyr Met Phe Glu Ser Lys Ser Met Lys Ile Arg	
350 355 360 365	
act caa ata cct gca gaa atg cta gca agc atc gat ttg aaa tac ttc	1333
Thr Gln Ile Pro Ala Glu Met Leu Ala Ser Ile Asp Leu Lys Tyr Phe	
370 375 380	
aat gat tca act aga aag aat gaa aaa atc cgg ccg ctc tta ata	1381
Asn Asp Ser Thr Arg Lys Lys Ile Glu Lys Ile Arg Pro Leu Leu Ile	
385 390 395	

gat ggg act gca tca ttg agc cct gga atg atg atg ggc atg ttc aat		1429	
Asp Gly Thr Ala Ser Leu Ser Pro Gly Met Met Met Gly Met Phe Asn			
400	405	410	
atg tta agt act gta tta ggc gtc tcc atc ctg aat ctt gga caa aag		1477	
Met Leu Ser Thr Val Leu Gly Val Ser Ile Leu Asn Leu Gly Gln Lys			
415	420	425	
aga cac acc aag act act tac tgg tgg gat ggt ctt caa tct tct gat		1525	
Arg His Thr Lys Thr Tyr Trp Trp Asp Gly Leu Gln Ser Ser Asp			
430	435	440	445
gat ttt gct ctg att gtg aat gca ccc aat cat gaa ggg att caa gcc		1573	
Asp Phe Ala Leu Ile Val Asn Ala Pro Asn His Glu Gly Ile Gln Ala			
450	455	460	
gga gtc aac agg ttt tat cga acc tgt aag cta ctt gga att aat atg		1621	
Gly Val Asn Arg Phe Tyr Arg Thr Cys Lys Leu Leu Gly Ile Asn Met			
465	470	475	
agc aag aaa aag tct tac ata aac aga aca ggt aca ttt gaa ttc aca		1669	
Ser Lys Lys Ser Tyr Ile Asn Arg Thr Gly Thr Phe Glu Phe Thr			
480	485	490	
agc ttt ttc tat cgt tat ggg ttt gtt gcc aat ttc agc atg gag ctt		1717	
Ser Phe Phe Tyr Arg Tyr Gly Phe Val Ala Asn Phe Ser Met Glu Leu			
495	500	505	
ccc agc ttt ggg gtg tct ggg atc aac gag tct gcg gac atg agt att		1765	
Pro Ser Phe Gly Val Ser Gly Ile Asn Glu Ser Ala Asp Met Ser Ile			
510	515	520	525
gga gtt act gtc atc aaa aac aat atg ata aac aat gat ctt ggt cca		1813	
Gly Val Thr Val Ile Lys Asn Asn Met Ile Asn Asn Asp Leu Gly Pro			
530	535	540	
gca acc gct caa atg gcc ctt cag ctg ttc atc aaa gat tac agg tac		1861	
Ala Thr Ala Gln Met Ala Leu Gln Leu Phe Ile Lys Asp Tyr Arg Tyr			
545	550	555	
acg tac cgg tgc cat aga ggt gac aca caa ata caa acc cga aga tca		1909	
Thr Tyr Arg Cys His Arg Gly Asp Thr Gln Ile Gln Thr Arg Arg Ser			
560	565	570	
ttt gaa ata aag aaa ctg tgg gag caa acc cat tcc aaa gct gga ctg		1957	
Phe Glu Ile Lys Lys Leu Trp Glu Gln Thr His Ser Lys Ala Gly Leu			
575	580	585	
ctg gtc tcc gac gga ggc cca aat tta tac aac att aga aat ctc cac		2005	
Leu Val Ser Asp Gly Gly Pro Asn Leu Tyr Asn Ile Arg Asn Leu His			
590	595	600	605
att cct gaa gtc tgc ttg aaa tgg gaa tta atg gat gag gat tac cag		2053	
Ile Pro Glu Val Cys Leu Lys Trp Glu Leu Met Asp Glu Asp Tyr Gln			
610	615	620	
ggg cgt tta tgc aac cca ctg aac cca ttt gtc aac cat aaa gac att		2101	
Gly Arg Leu Cys Asn Pro Leu Asn Pro Phe Val Asn His Lys Asp Ile			
625	630	635	
gaa tca gtg aac aat gca gtg ata atg cca gca cat ggt cca gcc aaa		2149	
Glu Ser Val Asn Asn Ala Val Ile Met Pro Ala His Gly Pro Ala Lys			
640	645	650	

aac atg gag tat gat gct gca aca aca cac tcc tgg atc ccc aaa	2197
Asn Met Glu Tyr Asp Ala Val Ala Thr Thr His Ser Trp Ile Pro Lys	
655 660 665	
aga aat cga tcc atc ttg aat aca agc caa aga gga ata ctt gaa gat	2245
Arg Asn Arg Ser Ile Leu Asn Thr Ser Gln Arg Gly Ile, Leu Glu Asp	
670 675 680 685	
gaa caa atg tac caa aag tgc tgc aac tta ttt gaa aaa ttc ttc ccc	2293
Glu Gln Met Tyr Gln Lys Cys Cys Asn Leu Phe Glu Lys Phe Phe Pro	
690 695 700	
agc agt tca tac aga aga cca gtc ggg ata tcc agt atg gtg gag gct	2341
Ser Ser Ser Tyr Arg Arg Pro Val Gly Ile Ser Ser Met Val Glu Ala	
705 710 715	
atg gtt tcc aga gcc cga att gat gca cga att gat ttc gaa tct gga	2389
Met Val Ser Arg Ala Arg Ile Asp Ala Arg Ile Asp Phe Glu Ser Gly	
720 725 730	
agg ata aag aaa gag gag ttc act gag atc atg aag atc tgt tcc acc	2437
Arg Ile Lys Lys Glu Glu Phe Thr Glu Ile Met Lys Ile Cys Ser Thr	
735 740 745	
att gaa gag ctc aga cgg caa aaa tagtgaattt agcttgcct tcataaaaaa	2491
Ile Glu Glu Leu Arg Arg Gln Lys	
750 755	
atgccttgtt tctactaata acccgccggc ccaaatgcc gactcggagc gaaagatata	2551
cctcccccgg ggccgggagg tcgcgtcacc gaccacgccc ccggcccagg cgacgcgcga	2611
cacggacacc tgcggccaaa aacgcccacca tcgcagccac acacggagcg cccggggccc	2671
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gccggccctt cctacgaccg ggacacacga gggaccgaag gccggccagg cgacgttct	2851
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tctgcgtc agtggaaacga aaactcacgt taaggattt tggtcatgag attatcaaaa	3691

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 aattctgttt tatcagaccg cttctgcgtt ctgatttat ctgtatcagg tggaaaatct 5131
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<210> 25

<211> 757

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: WSN-PB1

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Ala Ile Ser Thr Thr Phe Pro Tyr Thr Gly Asp Pro Pro Tyr Ser His
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Gly Thr Gly Thr Gly Tyr Thr Met Asp Thr Val Asn Arg Thr His Gln
 35 40 45

Tyr Ser Glu Arg Gly Arg Trp Thr Thr Asn Thr Glu Thr Gly Ala Pro
 50 55 60
 Gln Leu Asn Pro Ile Asp Gly Pro Leu Pro Glu Asp Asn Glu Pro Ser
 65 70 75 80
 Gly Tyr Ala Gln Thr Asp Cys Val Leu Glu Ala Met Ala Phe Leu Glu
 85 90 95
 Glu Ser His Pro Gly Ile Phe Glu Thr Ser Cys Leu Glu Thr Met Glu
 100 105 110
 Val Val Gln Gln Thr Arg Val Asp Lys Leu Thr Gln Gly Arg Gln Thr
 115 120 125
 Tyr Asp Trp Thr Leu Asn Arg Asn Gln Pro Ala Ala Thr Ala Leu Ala
 130 135 140
 Asn Thr Ile Glu Val Phe Arg Ser Asn Gly Leu Thr Ala Asn Glu Ser
 145 150 155 160
 Gly Arg Leu Ile Asp Phe Leu Lys Asp Val Met Glu Ser Met Asn Lys
 165 170 175
 Glu Glu Met Glu Ile Thr Thr His Phe Gln Arg Lys Arg Arg Val Arg
 180 185 190
 Asp Asn Met Thr Lys Lys Met Val Thr Gln Arg Thr Ile Gly Lys Arg
 195 200 205
 Lys Gln Arg Leu Asn Lys Arg Ser Tyr Leu Ile Arg Ala Leu Thr Leu
 210 215 220
 Asn Thr Met Thr Lys Asp Ala Glu Arg Gly Lys Leu Lys Arg Arg Ala
 225 230 235 240
 Ile Ala Thr Pro Gly Met Gln Ile Arg Gly Phe Val Tyr Phe Val Glu
 245 250 255
 Thr Leu Ala Arg Ser Ile Cys Glu Lys Leu Glu Gln Ser Gly Leu Pro
 260 265 270
 Val Gly Gly Asn Glu Lys Lys Ala Lys Leu Ala Asn Val Val Arg Lys
 275 280 285
 Met Met Thr Asn Ser Gln Asp Thr Glu Ile Ser Phe Thr Ile Thr Gly
 290 295 300
 Asp Asn Thr Lys Trp Asn Glu Asn Gln Asn Pro Arg Met Phe Leu Ala
 305 310 315 320
 Met Ile Thr Tyr Ile Thr Arg Asn Gln Pro Glu Trp Phe Arg Asn Val
 325 330 335
 Leu Ser Ile Ala Pro Ile Met Phe Ser Asn Lys Met Ala Arg Leu Gly
 340 345 350
 Lys Gly Tyr Met Phe Glu Ser Lys Ser Met Lys Ile Arg Thr Gln Ile
 355 360 365
 Pro Ala Glu Met Leu Ala Ser Ile Asp Leu Lys Tyr Phe Asn Asp Ser
 370 375 380
 Thr Arg Lys Lys Ile Glu Lys Ile Arg Pro Leu Leu Ile Asp Gly Thr
 385 390 395 400

Ala Ser Leu Ser Pro Gly Met Met Met Gly Met Phe Asn Met Leu Ser
 405 410 415
 Thr Val Leu Gly Val Ser Ile Leu Asn Leu Gly Gln Lys Arg His Thr
 420 425 430
 Lys Thr Thr Tyr Trp Trp Asp Gly Leu Gln Ser Ser Asp Asp Phe Ala
 435 440 445
 Leu Ile Val Asn Ala Pro Asn His Glu Gly Ile Gln Ala Gly Val Asn
 450 455 460
 Arg Phe Tyr Arg Thr Cys Lys Leu Leu Gly Ile Asn Met Ser Lys Lys
 465 470 475 480
 Lys Ser Tyr Ile Asn Arg Thr Gly Thr Phe Glu Phe Thr Ser Phe Phe
 485 490 495
 Tyr Arg Tyr Gly Phe Val Ala Asn Phe Ser Met Glu Leu Pro Ser Phe
 500 505 510
 Gly Val Ser Gly Ile Asn Glu Ser Ala Asp Met Ser Ile Gly Val Thr
 515 520 525
 Val Ile Lys Asn Asn Met Ile Asn Asn Asp Leu Gly Pro Ala Thr Ala
 530 535 540
 Gln Met Ala Leu Gln Leu Phe Ile Lys Asp Tyr Arg Tyr Thr Tyr Arg
 545 550 555 560
 Cys His Arg Gly Asp Thr Gln Ile Gln Thr Arg Arg Ser Phe Glu Ile
 565 570 575
 Lys Lys Leu Trp Glu Gln Thr His Ser Lys Ala Gly Leu Leu Val Ser
 580 585 590
 Asp Gly Gly Pro Asn Leu Tyr Asn Ile Arg Asn Leu His Ile Pro Glu
 595 600 605
 Val Cys Leu Lys Trp Glu Leu Met Asp Glu Asp Tyr Gln Gly Arg Leu
 610 615 620
 Cys Asn Pro Leu Asn Pro Phe Val Asn His Lys Asp Ile Glu Ser Val
 625 630 635 640
 Asn Asn Ala Val Ile Met Pro Ala His Gly Pro Ala Lys Asn Met Glu
 645 650 655
 Tyr Asp Ala Val Ala Thr Thr His Ser Trp Ile Pro Lys Arg Asn Arg
 660 665 670
 Ser Ile Leu Asn Thr Ser Gln Arg Gly Ile Leu Glu Asp Glu Gln Met
 675 680 685
 Tyr Gln Lys Cys Cys Asn Leu Phe Glu Lys Phe Phe Pro Ser Ser Ser
 690 695 700
 Tyr Arg Arg Pro Val Gly Ile Ser Ser Met Val Glu Ala Met Val Ser
 705 710 715 720
 Arg Ala Arg Ile Asp Ala Arg Ile Asp Phe Glu Ser Gly Arg Ile Lys
 725 730 735
 Lys Glu Glu Phe Thr Glu Ile Met Lys Ile Cys Ser Thr Ile Glu Glu
 740 745 750

Leu Arg Arg Gln Lys
755

<210> 26
<211> 5169
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: pHL3102

<220>
<221> CDS
<222> (191)..(2461)

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acaaagtgtc gcccggagta ctggtcgacc tccgaagttg ggggggagcg aaagcaggca 180
aaccatttga atg gat gtc aat ccg act tta ctt ttc tta aaa gtg cca 229
Met Asp Val Asn Pro Thr Leu Leu Phe Leu Lys Val Pro
1 5 10

gca caa aat gct ata agc aca act ttc cct tat act gga gac cct cct 277
Ala Gln Asn Ala Ile Ser Thr Thr Phe Pro Tyr Thr Gly Asp Pro Pro
15 20 25

tac agc cat ggg aca gga aca gga tac acc atg gat act gtc aac agg 325
Tyr Ser His Gly Thr Gly Thr Gly Tyr Thr Met Asp Thr Val Asn Arg
30 35 40 45

aca cat cag tac tca gaa agg gga aga tgg aca aca aac acc gaa act 373
Thr His Gln Tyr Ser Glu Arg Gly Arg Trp Thr Thr Asn Thr Glu Thr
50 55 60

gga gca ccg caa ctc aac ccg att gat ggg cca ctg cca gaa gac aat 421
Gly Ala Pro Gln Leu Asn Pro Ile Asp Gly Pro Leu Pro Glu Asp Asn
65 70 75

gaa cca agt ggt tat gcc caa aca gat tgt gta ttg gaa gca atg gcc 469
Glu Pro Ser Gly Tyr Ala Gln Thr Asp Cys Val Leu Glu Ala Met Ala
80 85 90

ttc ctt gag gaa tcc cat cct ggt atc ttt gag acc tcg tgt ctt gaa 517
Phe Leu Glu Glu Ser His Pro Gly Ile Phe Glu Thr Ser Cys Leu Glu
95 100 105

acg atg gag gtt gtt cag caa aca cga gtg gac aag ctg aca caa ggc 565
Thr Met Glu Val Val Gln Gln Thr Arg Val Asp Lys Leu Thr Gln Gly
110 115 120 125

cga cag acc tat gac tgg act cta aat agg aac cag cct gct gca aca 613
Arg Gln Thr Tyr Asp Trp Thr Leu Asn Arg Asn Gln Pro Ala Ala Thr
130 135 140

gca ttg gcc aac aca ata gaa gtg ttc aga tca aat ggc ctc acg gcc 661
Ala Leu Ala Asn Thr Ile Glu Val Phe Arg Ser Asn Gly Leu Thr Ala
145 150 155

aat gaa tct gga agg ctc ata gac ttc ctt aag gat gta atg gag tca 709
Asn Glu Ser Gly Arg Leu Ile Asp Phe Leu Lys Asp Val Met Glu Ser
160 165 170

atg aac aaa gaa gaa atg gag atc aca act cat ttt cag aga aag aga Met Asn Lys Glu Glu Met Glu Ile Thr Thr His Phe Gln Arg Lys Arg 175 180 185	757
cga gtg aga gac aat atg act aag aaa atg gtg aca cag aga aca ata Arg Val Arg Asp Asn Met Thr Lys Lys Met Val Thr Gln Arg Thr Ile 190 195 200 205	805
ggt aaa agg aag cag aga ttg aac aaa agg agt tat cta att agg gca Gly Lys Arg Lys Gln Arg Leu Asn Lys Arg Ser Tyr Leu Ile Arg Ala 210 215 220	853
tta acc ctg aac aca atg acc aaa gat gct gag aga ggg aag cta aaa Leu Thr Leu Asn Thr Met Thr Lys Asp Ala Glu Arg Gly Lys Leu Lys 225 230 235	901
cgg aga gca att gca acc cca ggg atg caa ata agg ggg ttt gta tac Arg Arg Ala Ile Ala Thr Pro Gly Met Gln Ile Arg Gly Phe Val Tyr 240 245 250	949
ttt gtt gag aca cta gca agg agt ata tgt gag aaa ctt gaa caa tca Phe Val Glu Thr Leu Ala Arg Ser Ile Cys Glu Lys Leu Glu Gln Ser 255 260 265	997
gga ttg cca gtt gga ggc aat gag aag aaa gca aag ttg gca aat gtt Gly Leu Pro Val Gly Gly Asn Glu Lys Lys Ala Lys Leu Ala Asn Val 270 275 280 285	1045
gta agg aag atg atg acc aat tct cag gac act gaa att tct ttc acc Val Arg Lys Met Met Thr Asn Ser Gln Asp Thr Glu Ile Ser Phe Thr 290 295 300	1093
atc act gga gat aac acc aaa tgg aac gaa aat cag aac cct cgg atg Ile Thr Gly Asp Asn Thr Lys Trp Asn Glu Asn Gln Asn Pro Arg Met 305 310 315	1141
ttt ttg gcc atg atc aca tat ata acc aga aat cag ccc gaa tgg ttc Phe Leu Ala Met Ile Thr Tyr Ile Thr Arg Asn Gln Pro Glu Trp Phe 320 325 330	1189
aga aat gtt cta agt att gct cca ata atg ttc tca aac aaa atg gcg Arg Asn Val Leu Ser Ile Ala Pro Ile Met Phe Ser Asn Lys Met Ala 335 340 345	1237
aga ctg gga aag ggg tac atg ttt gag agc aag agt atg aaa att aga Arg Leu Gly Lys Gly Tyr Met Phe Glu Ser Lys Ser Met Lys Ile Arg 350 355 360 365	1285
act caa ata cct gca gaa atg cta gca agc atc gat ttg aaa tac ttc Thr Gln Ile Pro Ala Glu Met Leu Ala Ser Ile Asp Leu Lys Tyr Phe 370 375 380	1333
aat gat tca act aga aag aag att gaa aaa atc cgg ccg ctc tta ata Asn Asp Ser Thr Arg Lys Lys Ile Glu Lys Ile Arg Pro Leu Leu Ile 385 390 395	1381
gat ggg act gca tca ttg agc cct gga atg atg atg ggc atg ttc aat Asp Gly Thr Ala Ser Leu Ser Pro Gly Met Met Met Gly Met Phe Asn 400 405 410	1429
atg tta agt act gta tta ggc gtc tcc atc ctg aat ctt gga caa aag Met Leu Ser Thr Val Leu Gly Val Ser Ile Leu Asn Leu Gly Gln Lys 415 420 425	1477
aga cac acc aag act act tac tgg tgg gat ggt ctt caa tct tct gat Arg His Thr Lys Thr Tyr Trp Trp Asp Gly Leu Gln Ser Ser Asp 430 435 440 445	1525

gat ttt gct ctg att gtg aat gca ccc aat cat gaa ggg att caa gcc Asp Phe Ala Leu Ile Val Asn Ala Pro Asn His Glu Gly Ile Gln Ala 450 455 460	1573
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gga gta aca gtg ata aag aat aac atg ata aac aat gat ctt gga ccg Gly Val Thr Val Ile Lys Asn Asn Met Ile Asn Asn Asp Leu Gly Pro 530 535 540	1813
gca aca gcc caa atg gct ctc caa tta ttc atc aag gac tac aga tat Ala Thr Ala Gln Met Ala Leu Gln Leu Phe Ile Lys Asp Tyr Arg Tyr 545 550 555	1861
aca tac agg tgt cac agg gga gac aca caa atc caa acg agg agg tca Thr Tyr Arg Cys His Arg Gly Asp Thr Gln Ile Gln Thr Arg Arg Ser 560 565 570	1909
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atc ccg gaa gtt tgc ctg aaa tgg gaa cta atg gat gaa gac tat cag Ile Pro Glu Val Cys Leu Lys Trp Glu Leu Met Asp Glu Asp Tyr Gln 610 615 620	2053
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 atg gtg tct agg gcc cg att gat gca cga att gac ttc gag tct gga 2389
 Met Val Ser Arg Ala Arg Ile Asp Ala Arg Ile Asp Phe Glu Ser Gly
 720 725 730

 agg att aag aag gaa gag ttt gct gag atc atg aag atc tgt tcc acc 2437
 Arg Ile Lys Lys Glu Glu Phe Ala Glu Ile Met Lys Ile Cys Ser Thr
 735 740 745

 att gaa gag ctc aga cg caa aaa tagtgaattt agcttgcct tcataaaaaa 2491
 Ile Glu Glu Leu Arg Arg Gln Lys
 750 755

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<211> 757

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: pHL3102

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Gly Thr Gly Thr Gly Tyr Thr Met Asp Thr Val Asn Arg Thr His Gln
 35 40 45

Tyr Ser Glu Arg Gly Arg Trp Thr Thr Asn Thr Glu Thr Gly Ala Pro
 50 55 60

Gln Leu Asn Pro Ile Asp Gly Pro Leu Pro Glu Asp Asn Glu Pro Ser
 65 70 75 80

Gly Tyr Ala Gln Thr Asp Cys Val Leu Glu Ala Met Ala Phe Leu Glu
 85 90 95

Glu Ser His Pro Gly Ile Phe Glu Thr Ser Cys Leu Glu Thr Met Glu
 100 105 110

Val Val Gln Gln Thr Arg Val Asp Lys Leu Thr Gln Gly Arg Gln Thr
 115 120 125
 Tyr Asp Trp Thr Leu Asn Arg Asn Gln Pro Ala Ala Thr Ala Leu Ala
 130 135 140
 Asn Thr Ile Glu Val Phe Arg Ser Asn Gly Leu Thr Ala Asn Glu Ser
 145 150 155 160
 Gly Arg Leu Ile Asp Phe Leu Lys Asp Val Met Glu Ser Met Asn Lys
 165 170 175
 Glu Glu Met Glu Ile Thr Thr His Phe Gln Arg Lys Arg Arg Val Arg
 180 185 190
 Asp Asn Met Thr Lys Lys Met Val Thr Gln Arg Thr Ile Gly Lys Arg
 195 200 205
 Lys Gln Arg Leu Asn Lys Arg Ser Tyr Leu Ile Arg Ala Leu Thr Leu
 210 215 220
 Asn Thr Met Thr Lys Asp Ala Glu Arg Gly Lys Leu Lys Arg Arg Ala
 225 230 235 240
 Ile Ala Thr Pro Gly Met Gln Ile Arg Gly Phe Val Tyr Phe Val Glu
 245 250 255
 Thr Leu Ala Arg Ser Ile Cys Glu Lys Leu Glu Gln Ser Gly Leu Pro
 260 265 270
 Val Gly Gly Asn Glu Lys Lys Ala Lys Leu Ala Asn Val Val Arg Lys
 275 280 285
 Met Met Thr Asn Ser Gln Asp Thr Glu Ile Ser Phe Thr Ile Thr Gly
 290 295 300
 Asp Asn Thr Lys Trp Asn Glu Asn Gln Asn Pro Arg Met Phe Leu Ala
 305 310 315 320
 Met Ile Thr Tyr Ile Thr Arg Asn Gln Pro Glu Trp Phe Arg Asn Val
 325 330 335
 Leu Ser Ile Ala Pro Ile Met Phe Ser Asn Lys Met Ala Arg Leu Gly
 340 345 350
 Lys Gly Tyr Met Phe Glu Ser Lys Ser Met Lys Ile Arg Thr Gln Ile
 355 360 365
 Pro Ala Glu Met Leu Ala Ser Ile Asp Leu Lys Tyr Phe Asn Asp Ser
 370 375 380
 Thr Arg Lys Lys Ile Glu Lys Ile Arg Pro Leu Leu Ile Asp Gly Thr
 385 390 395 400
 Ala Ser Leu Ser Pro Gly Met Met Gly Met Phe Asn Met Leu Ser
 405 410 415
 Thr Val Leu Gly Val Ser Ile Leu Asn Leu Gly Gln Lys Arg His Thr
 420 425 430
 Lys Thr Thr Tyr Trp Trp Asp Gly Leu Gln Ser Ser Asp Asp Phe Ala
 435 440 445
 Leu Ile Val Asn Ala Pro Asn His Glu Gly Ile Gln Ala Gly Val Asn
 450 455 460

Arg Phe Tyr Arg Thr Cys Lys Leu Leu Gly Ile Asn Met Ser Lys Lys
 465 470 475 480

Lys Ser Tyr Ile Asn Arg Thr Gly Thr Phe Glu Phe Thr Ser Phe Phe
 485 490 495

Tyr Arg Tyr Gly Phe Val Ala Asn Phe Ser Met Glu Leu Pro Ser Phe
 500 505 510

Gly Val Ser Gly Ile Asn Glu Ser Ala Asp Met Ser Ile Gly Val Thr
 515 520 525

Val Ile Lys Asn Asn Met Ile Asn Asn Asp Leu Gly Pro Ala Thr Ala
 530 535 540

Gln Met Ala Leu Gln Leu Phe Ile Lys Asp Tyr Arg Tyr Thr Tyr Arg
 545 550 555 560

Cys His Arg Gly Asp Thr Gln Ile Gln Thr Arg Arg Ser Phe Glu Leu
 565 570 575

Lys Lys Leu Trp Glu Gln Thr Arg Ser Lys Ala Gly Leu Leu Val Ser
 580 585 590

Asp Gly Gly Pro Asn Leu Tyr Asn Ile Arg Asn Leu His Ile Pro Glu
 595 600 605

Val Cys Leu Lys Trp Glu Leu Met Asp Glu Asp Tyr Gln Gly Arg Leu
 610 615 620

Cys Asn Pro Met Asn Pro Phe Val Ser His Lys Glu Ile Glu Ser Val
 625 630 635 640

Asn Asn Ala Ala Val Met Pro Ala His Gly Pro Ala Lys Ser Met Glu
 645 650 655

Tyr Asp Ala Val Ala Thr Thr His Ser Trp Ile Pro Lys Arg Asn Arg
 660 665 670

Ser Ile Leu Asn Thr Ser Gln Arg Gly Ile Leu Glu Asp Glu Gln Met
 675 680 685

Tyr Gln Lys Cys Cys Asn Leu Phe Glu Lys Phe Phe Pro Ser Ser Ser
 690 695 700

Tyr Arg Arg Pro Val Gly Ile Ser Ser Met Val Glu Ala Met Val Ser
 705 710 715 720

Arg Ala Arg Ile Asp Ala Arg Ile Asp Phe Glu Ser Gly Arg Ile Lys
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Lys Glu Glu Phe Ala Glu Ile Met Lys Ile Cys Ser Thr Ile Glu Glu
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Leu Arg Arg Gln Lys
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 <211> 5169
 <212> DNA
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<220>
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 acaaagtgtc gcccggagta ctggtcgacc tccgaagttg ggggggagcg aaagcaggca 180
 aaccatttga atg gat gtc aat ccg act tta ctg ttc ttg aaa gtt cct 229
 Met Asp Val Asn Pro Thr Leu Leu Phe Leu Lys Val Pro
 1 5 10

gcg caa aat gca ata agt act acg ttc cct tac act gga gat cct cca 277
 Ala Gln Asn Ala Ile Ser Thr Thr Phe Pro Tyr Thr Gly Asp Pro Pro
 15 20 25

tac agc cat gga aca ggg aca gga tac acc atg gac aca gtc aac agg 325
 Tyr Ser His Gly Thr Gly Thr Gly Tyr Thr Met Asp Thr Val Asn Arg
 30 35 40 45

aca cac caa tat tcg gaa aag ggg aaa tgg aca aca aac act gag act 373
 Thr His Gln Tyr Ser Glu Lys Gly Lys Trp Thr Thr Asn Thr Glu Thr
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gga gca ccc caa ctt aat cca att gat ggc cca ttg cct gag gac aat 421
 Gly Ala Pro Gln Leu Asn Pro Ile Asp Gly Pro Leu Pro Glu Asp Asn
 65 70 75

gaa cca agt gga tat gca caa aca gac tgc gtc ctg gaa gca atg gct 469
 Glu Pro Ser Gly Tyr Ala Gln Thr Asp Cys Val Leu Glu Ala Met Ala
 80 85 90

ttc ctt gaa gaa tcc cat cca gga atc ttt gaa aac tcg tgt ctt gag 517
 Phe Leu Glu Glu Ser His Pro Gly Ile Phe Glu Asn Ser Cys Leu Glu
 95 100 105

acg atg gaa gtt gtt caa caa aca aga gtg gac aaa ctg acc caa ggc 565
 Thr Met Glu Val Val Gln Gln Thr Arg Val Asp Lys Leu Thr Gln Gly
 110 115 120 125

cgt cag act tat gat tgg act ttg aat aga aac cag cct gct gca act 613
 Arg Gln Thr Tyr Asp Trp Thr Leu Asn Arg Asn Gln Pro Ala Ala Thr
 130 135 140

gca tta gca aac act ata gag gtc ttt aga tcg aat ggt cta aca gct 661
 Ala Leu Ala Asn Thr Ile Glu Val Phe Arg Ser Asn Gly Leu Thr Ala
 145 150 155

aat gaa tca ggg agg ctc ata gat ttc ctc aag gat gtg atg gaa tca 709
 Asn Glu Ser Gly Arg Leu Ile Asp Phe Leu Lys Asp Val Met Glu Ser
 160 165 170

atg gat aag gag gaa atg gag ata aca aca cat ttc caa cga aag aga 757
 Met Asp Lys Glu Glu Met Glu Ile Thr Thr His Phe Gln Arg Lys Arg
 175 180 185

aga gta aga gac aac atg acc aag aaa atg gtc aca caa aga aca ata 805
 Arg Val Arg Asp Asn Met Thr Lys Lys Met Val Thr Gln Arg Thr Ile
 190 195 200 205

ggg aag aaa aag cag aga ctt aac aaa agg agc tac cta ata agg gct 853
 Gly Lys Lys Gln Arg Leu Asn Lys Arg Ser Tyr Leu Ile Arg Ala
 210 215 220

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gac ggc aca gcc tca tta agc ccg gga atg atg atg ggt atg ttc aac Asp Gly Thr Ala Ser Leu Ser Pro Gly Met Met Met Gly Met Phe Asn 400 405 410	1429
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aga tac acc aaa acc aca tac tgg tgg gat gga ctt cag tcc tct gat Arg Tyr Thr Lys Thr Tyr Trp Trp Asp Gly Leu Gln Ser Ser Asp 430 435 440 445	1525
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Pro Ser Phe Gly Val Ser Gly Ile Asn Glu Ser Ala Asp Met Ser Ile		
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Ala Thr Ala Gln Met Ala Leu Gln Leu Phe Ile Lys Asp Tyr Arg Tyr		
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670 675 680 685		
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Met Val Ser Arg Ala Arg Ile Asp Ala Arg Ile Asp Phe Glu Ser Gly		
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735 740 745		

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 Ile Glu Glu Leu Arg Arg Gln Lys
 750 755

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<210> 29

<211> 757

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: pH3103

<400> 29

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Tyr	Ser	Glu	Lys	Gly	Lys	Trp	Thr	Thr	Asn	Thr	Glu	Thr	Gly	Ala	Pro
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Gln	Leu	Asn	Pro	Ile	Asp	Gly	Pro	Leu	Pro	Glu	Asp	Asn	Glu	Pro	Ser
65							70			75			80		

Gly	Tyr	Ala	Gln	Thr	Asp	Cys	Val	Leu	Glu	Ala	Met	Ala	Phe	Leu	Glu
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Glu	Ser	His	Pro	Gly	Ile	Phe	Glu	Asn	Ser	Cys	Leu	Glu	Thr	Met	Glu
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Val	Val	Gln	Gln	Thr	Arg	Val	Asp	Lys	Leu	Thr	Gln	Gly	Arg	Gln	Thr
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Tyr	Asp	Trp	Thr	Leu	Asn	Arg	Asn	Gln	Pro	Ala	Ala	Thr	Ala	Leu	Ala
130							135				140				

Asn	Thr	Ile	Glu	Val	Phe	Arg	Ser	Asn	Gly	Leu	Thr	Ala	Asn	Glu	Ser
145							150			155		160			

Gly	Arg	Leu	Ile	Asp	Phe	Leu	Lys	Asp	Val	Met	Glu	Ser	Met	Asp	Lys
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Glu Glu Met Glu Ile Thr Thr His Phe Gln Arg Lys Arg Arg Val Arg
 180 185 190
 Asp Asn Met Thr Lys Lys Met Val Thr Gln Arg Thr Ile Gly Lys Lys
 195 200 205
 Lys Gln Arg Leu Asn Lys Arg Ser Tyr Leu Ile Arg Ala Leu Thr Leu
 210 215 220
 Asn Thr Met Thr Lys Asp Ala Glu Arg Gly Lys Leu Lys Arg Arg Ala
 225 230 235 240
 Ile Ala Thr Pro Gly Met Gln Ile Arg Gly Phe Val Tyr Phe Val Glu
 245 250 255
 Thr Leu Ala Arg Ser Ile Cys Glu Lys Leu Glu Gln Ser Gly Leu Pro
 260 265 270
 Val Gly Gly Asn Glu Lys Lys Ala Lys Leu Ala Asn Val Val Arg Lys
 275 280 285
 Met Met Thr Asn Ser Gln Asp Thr Glu Leu Ser Phe Thr Ile Thr Gly
 290 295 300
 Asp Asn Thr Lys Trp Asn Glu Asn Gln Asn Pro Arg Met Phe Leu Ala
 305 310 315 320
 Met Ile Thr Tyr Ile Thr Arg Asn Gln Pro Glu Trp Phe Arg Asn Val
 325 330 335
 Leu Ser Ile Ala Pro Ile Met Phe Ser Asn Lys Met Ala Arg Leu Gly
 340 345 350
 Lys Gly Tyr Met Phe Glu Ser Lys Ser Met Lys Leu Arg Thr Gln Ile
 355 360 365
 Pro Ala Glu Met Leu Ala Ser Ile Asp Leu Lys Tyr Phe Asn Glu Pro
 370 375 380
 Thr Arg Lys Lys Ile Glu Lys Ile Arg Pro Leu Ile Ile Asp Gly Thr
 385 390 395 400
 Ala Ser Leu Ser Pro Gly Met Met Gly Met Phe Asn Met Leu Ser
 405 410 415
 Thr Val Leu Gly Val Ser Ile Leu Asn Leu Gly Gln Lys Arg Tyr Thr
 420 425 430
 Lys Thr Thr Tyr Trp Trp Asp Gly Leu Gln Ser Ser Asp Asp Phe Ala
 435 440 445
 Leu Ile Val Asn Ala Pro Asn His Glu Gly Ile Gln Ala Gly Val Asp
 450 455 460
 Arg Phe Tyr Arg Thr Cys Lys Leu Val Gly Ile Asn Met Ser Lys Lys
 465 470 475 480
 Lys Ser Tyr Ile Asn Arg Thr Gly Thr Phe Glu Phe Thr Ser Phe Phe
 485 490 495
 Tyr Arg Tyr Gly Phe Val Ala Asn Phe Ser Met Glu Leu Pro Ser Phe
 500 505 510
 Gly Val Ser Gly Ile Asn Glu Ser Ala Asp Met Ser Ile Gly Val Thr
 515 520 525

Val Ile Lys Asn Asn Met Ile Asn Asn Asp Leu Gly Pro Ala Thr Ala
 530 535 540
 Gln Met Ala Leu Gln Leu Phe Ile Lys Asp Tyr Arg Tyr Thr Tyr Arg
 545 550 555 560
 Cys His Arg Gly Asp Thr Gln Ile Gln Thr Arg Arg Ser Phe Glu Ile
 565 570 575
 Lys Lys Leu Trp Glu Gln Thr His Ser Lys Ala Gly Leu Leu Val Ser
 580 585 590
 Asp Gly Gly Pro Asn Leu Tyr Asn Ile Arg Asn Leu His Ile Pro Glu
 595 600 605
 Val Cys Leu Lys Trp Glu Leu Met Asp Glu Asp Tyr Gln Gly Arg Leu
 610 615 620
 Cys Asn Pro Leu Asn Pro Phe Val Asn His Lys Asp Ile Glu Ser Val
 625 630 635 640
 Asn Asn Ala Val Ile Met Pro Ala His Gly Pro Ala Lys Asn Met Glu
 645 650 655
 Tyr Asp Ala Val Ala Thr Thr His Ser Trp Ile Pro Lys Arg Asn Arg
 660 665 670
 Ser Ile Leu Asn Thr Ser Gln Arg Gly Ile Leu Glu Asp Glu Gln Met
 675 680 685
 Tyr Gln Lys Cys Cys Asn Leu Phe Glu Lys Phe Phe Pro Ser Ser Ser
 690 695 700
 Tyr Arg Arg Pro Val Gly Ile Ser Ser Met Val Glu Ala Met Val Ser
 705 710 715 720
 Arg Ala Arg Ile Asp Ala Arg Ile Asp Phe Glu Ser Gly Arg Ile Lys
 725 730 735
 Lys Glu Glu Phe Thr Glu Ile Met Lys Ile Cys Ser Thr Ile Glu Glu
 740 745 750
 Leu Arg Arg Gln Lys
 755

<210> 30
 <211> 5169
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: pHL3130

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 acaaagtgtc gcccggagta ctggtcgacc tccgaagttg ggggggagcg aaagcaggca 180

aaccatttga atg gat gtc aat ccg act tta ctt ttc tta aaa gtg cca	229
Met Asp Val Asn Pro Thr Leu Leu Phe Leu Lys Val Pro	
1 5 10	
gca caa aat gct ata agc aca act ttc cct tat act gga gac cct cct	277
Ala Gln Asn Ala Ile Ser Thr Thr Phe Pro Tyr Thr Gly Asp Pro Pro	
15 20 25	
tac agc cat ggg aca gga aca gga tac acc atg gat act gtc aac agg	325
Tyr Ser His Gly Thr Gly Thr Gly Tyr Thr Met Asp Thr Val Asn Arg	
30 35 40 45	
aca cat cag tac tca gaa agg gga aga tgg aca aca aac acc gaa act	373
Thr His Gln Tyr Ser Glu Arg Gly Arg Trp Thr Thr Asn Thr Glu Thr	
50 55 60	
gga gca ccg caa ctc aac ccg att gat ggg cca ctg cca gaa gac aat	421
Gly Ala Pro Gln Leu Asn Pro Ile Asp Gly Pro Leu Pro Glu Asp Asn	
65 70 75	
gaa cca agt ggt tat gcc caa aca gat tgt gta ttg gaa gca atg gcc	469
Glu Pro Ser Gly Tyr Ala Gln Thr Asp Cys Val Leu Glu Ala Met Ala	
80 85 90	
ttc ctt gag gaa tcc cat cct ggt atc ttt gag acc tcg tgt ctt gaa	517
Phe Leu Glu Glu Ser His Pro Gly Ile Phe Glu Thr Ser Cys Leu Glu	
95 100 105	
acg atg gag gtt gtt cag caa aca cga gtg gac aag ctg aca caa ggc	565
Thr Met Glu Val Val Gln Gln Thr Arg Val Asp Lys Leu Thr Gln Gly	
110 115 120 125	
cga cag acc tat gac tgg act cta aat agg aac cag cct gct gca aca	613
Arg Gln Thr Tyr Asp Trp Thr Leu Asn Arg Asn Gln Pro Ala Ala Thr	
130 135 140	
gca ttg gcc aac aca ata gaa gtg ttc aga tca aat ggc ctc acg gcc	661
Ala Leu Ala Asn Thr Ile Glu Val Phe Arg Ser Asn Gly Leu Thr Ala	
145 150 155	
aat gaa tct gga agg ctc ata gac ttc ctt aag gat gta atg gag tca	709
Asn Glu Ser Gly Arg Leu Ile Asp Phe Leu Lys Asp Val Met Glu Ser	
160 165 170	
atg aac aaa gaa gaa atg gag atc aca act cat ttt cag aga aag aga	757
Met Asn Lys Glu Glu Met Glu Ile Thr Thr His Phe Gln Arg Lys Arg	
175 180 185	
cga gtg aga gac aat atg act aag aaa atg gtg aca cag aga aca ata	805
Arg Val Arg Asp Asn Met Thr Lys Lys Met Val Thr Gln Arg Thr Ile	
190 195 200 205	
ggt aaa agg aag cag aga ttg aac aaa agg agt tat cta att agg gca	853
Gly Lys Arg Lys Gln Arg Leu Asn Lys Arg Ser Tyr Leu Ile Arg Ala	
210 215 220	
tta acc ctg aac aca atg acc aaa gat gct gag aga ggg aag cta aaa	901
Leu Thr Leu Asn Thr Met Thr Lys Asp Ala Glu Arg Gly Lys Leu Lys	
225 230 235	
cgg aga gca att gca aca cca ggg atg cag atc aga ggg ttt gtg tac	949
Arg Arg Ala Ile Ala Thr Pro Gly Met Gln Ile Arg Gly Phe Val Tyr	
240 245 250	
ttt gtt gag aca ctg gcg aga agc att tgc gag aag ctt gaa cag tct	997
Phe Val Glu Thr Leu Ala Arg Ser Ile Cys Glu Lys Leu Glu Gln Ser	
255 260 265	

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Gly Leu Pro Val Gly Gly Asn Glu Lys Lys Ala Lys Leu Ala Asn Val		
270 275 280 285		
gtg agg aag atg atg acg aac tca caa gac act gag ctc tct ttc aca		1093
Val Arg Lys Met Met Thr Asn Ser Gln Asp Thr Glu Leu Ser Phe Thr		
290 295 300		
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Ile Thr Gly Asp Asn Thr Lys Trp Asn Glu Asn Gln Asn Pro Arg Met		
305 310 315		
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Phe Leu Ala Met Ile Thr Tyr Ile Thr Arg Asn Gln Pro Glu Trp Phe		
320 325 330		
aga aat gtc ttg agc atc gcg ccg ata atg ttt tcg aac aaa atg gcg		1237
Arg Asn Val Leu Ser Ile Ala Pro Ile Met Phe Ser Asn Lys Met Ala		
335 340 345		
agg cta ggg aaa ggg tac atg ttc gaa agc aaa agc atg aag ctc cga		1285
Arg Leu Gly Lys Gly Tyr Met Phe Glu Ser Lys Ser Met Lys Leu Arg		
350 355 360 365		
aca caa ata cca gca gaa atg cta gca agt att gat cta aaa tat ttc		1333
Thr Gln Ile Pro Ala Glu Met Leu Ala Ser Ile Asp Leu Lys Tyr Phe		
370 375 380		
aat gaa cca aca agg aag aaa atc gag aaa ata agg cct ctc ata ata		1381
Asn Glu Pro Thr Arg Lys Lys Ile Glu Lys Ile Arg Pro Leu Ile Ile		
385 390 395		
gac ggc aca gcc tca tta agc ccg gga atg atg atg ggt atg ttc aac		1429
Asp Gly Thr Ala Ser Leu Ser Pro Gly Met Met Met Gly Met Phe Asn		
400 405 410		
atg ctg agt aca gtg ttg gga gtc tca atc ctg aat ctt ggg caa aag		1477
Met Leu Ser Thr Val Leu Gly Val Ser Ile Leu Asn Leu Gly Gln Lys		
415 420 425		
aga tac acc aaa acc aca tac tgg tgg gat gga ctt cag tcc tct gat		1525
Arg Tyr Thr Lys Thr Tyr Trp Trp Asp Gly Leu Gln Ser Ser Asp		
430 435 440 445		
gat ttt gct ctc atc gtg aat gca cca aat cat gag gga ata caa gcg		1573
Asp Phe Ala Leu Ile Val Asn Ala Pro Asn His Glu Gly Ile Gln Ala		
450 455 460		
gga gtg gat aga ttc tac aga acc tgc aag cta gtt ggg atc aat atg		1621
Gly Val Asp Arg Phe Tyr Arg Thr Cys Lys Leu Val Gly Ile Asn Met		
465 470 475		
agc aag aaa aag tcc tat ata aat agg aca gga aca ttc gaa ttc aca		1669
Ser Lys Lys Ser Tyr Ile Asn Arg Thr Gly Thr Phe Glu Phe Thr		
480 485 490		
agc ttt ttc tac cgc tat gga ttt gta gcc aat ttt agt atg gag ttg		1717
Ser Phe Phe Tyr Arg Tyr Gly Phe Val Ala Asn Phe Ser Met Glu Leu		
495 500 505		
ccc agc ttt gga gta tca gga att aat gaa tcg gct gat atg agc att		1765
Pro Ser Phe Gly Val Ser Gly Ile Asn Glu Ser Ala Asp Met Ser Ile		
510 515 520 525		

gga gta aca gtg ata aag aat aac atg ata aac aat gat ctt gga ccg	530	535	540	1813
Gly Val Thr Val Ile Lys Asn Asn Met Ile Asn Asn Asp Leu Gly Pro				
gca aca gcc caa atg gct ctc caa tta ttc atc aag gac tac aga tat	545	550	555	1861
Ala Thr Ala Gln Met Ala Leu Gln Leu Phe Ile Lys Asp Tyr Arg Tyr				
aca tac agg tgt cac agg gga gac aca caa atc caa acg agg agg tca	560	565	570	1909
Thr Tyr Arg Cys His Arg Gly Asp Thr Gln Ile Gln Thr Arg Arg Ser				
ttc gag cta aag aag ctg tgg gag cag acc cgc tca aag gca gga ctg	575	580	585	1957
Phe Glu Leu Lys Lys Leu Trp Glu Gln Thr Arg Ser Lys Ala Gly Leu				
ttg gtt tca gat ggc gga cca aac ctg tac aac att cgg aat ctc cac	590	595	600	2003
Leu Val Ser Asp Gly Gly Pro Asn Leu Tyr Asn Ile Arg Asn Leu His				
atc ccg gaa gtt tgc ctg aaa tgg gaa cta atg gat gaa gac tat cag	610	615	620	2053
Ile Pro Glu Val Cys Leu Lys Trp Glu Leu Met Asp Glu Asp Tyr Gln				
gga aga ctt tgt aat ccc atg aac ccg ttt gtc agt cat aag gaa att	625	630	635	2101
Gly Arg Leu Cys Asn Pro Met Asn Pro Phe Val Ser His Lys Glu Ile				
gaa tct gta aac aat gct gcg gta atg cca gcc cat ggt cca gcc aaa	640	645	650	2149
Glu Ser Val Asn Asn Ala Ala Val Met Pro Ala His Gly Pro Ala Lys				
agc atg gaa tat gat gct gtg gca act aca cac tct tgg atc cct aag	655	660	665	2197
Ser Met Glu Tyr Asp Ala Val Ala Thr Thr His Ser Trp Ile Pro Lys				
aga aac cgt tcc att ctc aat acg agt caa agg gga atc ctt gag gat	670	675	680	2243
Arg Asn Arg Ser Ile Leu Asn Thr Ser Gln Arg Gly Ile Leu Glu Asp				
gaa caa atg tac cag aag tgt tgc aac cta ttc gag aaa ttc ttc cct	690	695	700	2293
Glu Gln Met Tyr Gln Lys Cys Cys Asn Leu Phe Glu Lys Phe Phe Pro				
agc agc tca tac aga aga cca gtt gga att tcc agt atg gtg gag gcc	705	710	715	2341
Ser Ser Ser Tyr Arg Arg Pro Val Gly Ile Ser Ser Met Val Glu Ala				
atg gtg tct agg gcc cggtt att gat gca cga att gac ttc gag tct gga	720	725	730	2389
Met Val Ser Arg Ala Arg Ile Asp Ala Arg Ile Asp Phe Glu Ser Gly				
agg att aag aag gaa gag ttt gct gag atc atg aag atc tgt tcc acc	735	740	745	2437
Arg Ile Lys Lys Glu Glu Phe Ala Glu Ile Met Lys Ile Cys Ser Thr				
att gaa gag ctc aga cgg caa aaa tagtgaattt agcttgcct tcataaaaaa	750	755		2491
Ile Glu Glu Leu Arg Arg Gln Lys				
atgccttgtt tctactaata acccgccggc ccaaaatgcc gactcggagc gaaagatata				2551
cctcccccgg ggccgggagg tcgcgtcacc gaccacgccc ccggccccagg cgacgcgcga				2611
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tctggtcaac cccaggacac acgcgggagc agcgccgggc cggggacgccc ctccccggccg				2731

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<210> 31

<211> 757

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: pH3130

<400> 31

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Gly Thr Gly Thr Gly Tyr Thr Met Asp Thr Val Asn Arg Thr His Gln
 35 40 45

Tyr Ser Glu Arg Gly Arg Trp Thr Thr Asn Thr Glu Thr Gly Ala Pro
 50 55 60

Gln Leu Asn Pro Ile Asp Gly Pro Leu Pro Glu Asp Asn Glu Pro Ser
 65 70 75 80

Gly Tyr Ala Gln Thr Asp Cys Val Leu Glu Ala Met Ala Phe Leu Glu
 85 90 95

Glu Ser His Pro Gly Ile Phe Glu Thr Ser Cys Leu Glu Thr Met Glu
 100 105 110

Val Val Gln Gln Thr Arg Val Asp Lys Leu Thr Gln Gly Arg Gln Thr
 115 120 125

Tyr Asp Trp Thr Leu Asn Arg Asn Gln Pro Ala Ala Thr Ala Leu Ala
 130 135 140

Asn Thr Ile Glu Val Phe Arg Ser Asn Gly Leu Thr Ala Asn Glu Ser
 145 150 155 160

Gly Arg Leu Ile Asp Phe Leu Lys Asp Val Met Glu Ser Met Asn Lys
 165 170 175

Glu Glu Met Glu Ile Thr Thr His Phe Gln Arg Lys Arg Arg Val Arg
 180 185 190

Asp Asn Met Thr Lys Lys Met Val Thr Gln Arg Thr Ile Gly Lys Arg
 195 200 205

Lys Gln Arg Leu Asn Lys Arg Ser Tyr Leu Ile Arg Ala Leu Thr Leu
 210 215 220

Asn Thr Met Thr Lys Asp Ala Glu Arg Gly Lys Leu Lys Arg Arg Ala
 225 230 235 240
 Ile Ala Thr Pro Gly Met Gln Ile Arg Gly Phe Val Tyr Phe Val Glu
 245 250 255
 Thr Leu Ala Arg Ser Ile Cys Glu Lys Leu Glu Gln Ser Gly Leu Pro
 260 265 270
 Val Gly Gly Asn Glu Lys Lys Ala Lys Leu Ala Asn Val Val Arg Lys
 275 280 285
 Met Met Thr Asn Ser Gln Asp Thr Glu Leu Ser Phe Thr Ile Thr Gly
 290 295 300
 Asp Asn Thr Lys Trp Asn Glu Asn Gln Asn Pro Arg Met Phe Leu Ala
 305 310 315 320
 Met Ile Thr Tyr Ile Thr Arg Asn Gln Pro Glu Trp Phe Arg Asn Val
 325 330 335
 Leu Ser Ile Ala Pro Ile Met Phe Ser Asn Lys Met Ala Arg Leu Gly
 340 345 350
 Lys Gly Tyr Met Phe Glu Ser Lys Ser Met Lys Leu Arg Thr Gln Ile
 355 360 365
 Pro Ala Glu Met Leu Ala Ser Ile Asp Leu Lys Tyr Phe Asn Glu Pro
 370 375 380
 Thr Arg Lys Lys Ile Glu Lys Ile Arg Pro Leu Ile Ile Asp Gly Thr
 385 390 395 400
 Ala Ser Leu Ser Pro Gly Met Met Met Gly Met Phe Asn Met Leu Ser
 405 410 415
 Thr Val Leu Gly Val Ser Ile Leu Asn Leu Gly Gln Lys Arg Tyr Thr
 420 425 430
 Lys Thr Thr Tyr Trp Trp Asp Gly Leu Gln Ser Ser Asp Asp Phe Ala
 435 440 445
 Leu Ile Val Asn Ala Pro Asn His Glu Gly Ile Gln Ala Gly Val Asp
 450 455 460
 Arg Phe Tyr Arg Thr Cys Lys Leu Val Gly Ile Asn Met Ser Lys Lys
 465 470 475 480
 Lys Ser Tyr Ile Asn Arg Thr Gly Thr Phe Glu Phe Thr Ser Phe Phe
 485 490 495
 Tyr Arg Tyr Gly Phe Val Ala Asn Phe Ser Met Glu Leu Pro Ser Phe
 500 505 510
 Gly Val Ser Gly Ile Asn Glu Ser Ala Asp Met Ser Ile Gly Val Thr
 515 520 525
 Val Ile Lys Asn Asn Met Ile Asn Asn Asp Leu Gly Pro Ala Thr Ala
 530 535 540
 Gln Met Ala Leu Gln Leu Phe Ile Lys Asp Tyr Arg Tyr Thr Tyr Arg
 545 550 555 560
 Cys His Arg Gly Asp Thr Gln Ile Gln Thr Arg Arg Ser Phe Glu Leu
 565 570 575

Lys Lys Leu Trp Glu Gln Thr Arg Ser Lys Ala Gly Leu Leu Val Ser
 580 585 590

Asp Gly Gly Pro Asn Leu Tyr Asn Ile Arg Asn Leu His Ile Pro Glu
 595 600 605

Val Cys Leu Lys Trp Glu Leu Met Asp Glu Asp Tyr Gln Gly Arg Leu
 610 615 620

Cys Asn Pro Met Asn Pro Phe Val Ser His Lys Glu Ile Glu Ser Val
 625 630 635 640

Asn Asn Ala Ala Val Met Pro Ala His Gly Pro Ala Lys Ser Met Glu
 645 650 655

Tyr Asp Ala Val Ala Thr Thr His Ser Trp Ile Pro Lys Arg Asn Arg
 660 665 670

Ser Ile Leu Asn Thr Ser Gln Arg Gly Ile Leu Glu Asp Glu Gln Met
 675 680 685

Tyr Gln Lys Cys Cys Asn Leu Phe Glu Lys Phe Phe Pro Ser Ser Ser
 690 695 700

Tyr Arg Arg Pro Val Gly Ile Ser Ser Met Val Glu Ala Met Val Ser
 705 710 715 720

Arg Ala Arg Ile Asp Ala Arg Ile Asp Phe Glu Ser Gly Arg Ile Lys
 725 730 735

Lys Glu Glu Phe Ala Glu Ile Met Lys Ile Cys Ser Thr Ile Glu Glu
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Leu Arg Arg Gln Lys
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<210> 32

<211> 5169

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: pHL3131

<220>

<221> CDS

<222> (191)..(2461)

<400> 32

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acaaaagtgtc gcccggagta ctggtcgacc tccgaagttt ggggggagcgc aaagcaggca 180

aaccatttga atg gat gtc aat ccg act tta ctt ttc tta aaa gtg cca 229
 Met Asp Val Asn Pro Thr Leu Leu Phe Leu Lys Val Pro
 1 5 10

gca caa aat gct ata agc aca act ttc cct tat act gga gac cct cct 277
 Ala Gln Asn Ala Ile Ser Thr Thr Phe Pro Tyr Thr Gly Asp Pro Pro
 15 20 25

tac agc cat ggg aca gga aca gga tac acc atg gat act gtc aac agg 325
 Tyr Ser His Gly Thr Gly Thr Gly Tyr Thr Met Asp Thr Val Asn Arg
 30 35 40 45

aca cat cag tac tca gaa agg gga aga tgg aca aca aac acc gaa act	373
Thr His Gln Tyr Ser Glu Arg Gly Arg Trp Thr Thr Asn Thr Glu Thr	
50 55 60	
gga gca ccg caa ctc aac ccg att gat ggg cca ctg cca gaa gac aat	421
Gly Ala Pro Gin Leu Asn Pro Ile Asp Gly Pro Leu Pro Glu Asp Asn	
65 70 75	
gaa cca agt ggt tat gcc caa aca gat tgg gta ttg gaa gca atg gcc	469
Glu Pro Ser Gly Tyr Ala Gln Thr Asp Cys Val Leu Glu Ala Met Ala	
80 85 90	
tcc ctt gag gaa tcc cat cct ggt atc ttt gag acc tcg tgg ctt gaa	517
Phe Leu Glu Glu Ser His Pro Gly Ile Phe Glu Thr Ser Cys Leu Glu	
95 100 105	
acg atg gag gtt gtt cag caa aca cga gtg gac aag ctg aca caa ggc	565
Thr Met Glu Val Val Gln Gln Thr Arg Val Asp Lys Leu Thr Gln Gly	
110 115 120 125	
cga cag acc tat gac tgg act cta aat agg aac cag cct gct gca aca	613
Arg Gln Thr Tyr Asp Trp Thr Leu Asn Arg Asn Gln Pro Ala Ala Thr	
130 135 140	
gca ttg gcc aac aca ata gaa gtg ttc aga tca aat ggc ctc acg gcc	661
Ala Leu Ala Asn Thr Ile Glu Val Phe Arg Ser Asn Gly Leu Thr Ala	
145 150 155	
aat gaa tct gga agg ctc ata gac ttc ctt aag gat gta atg gag tca	709
Asn Glu Ser Gly Arg Leu Ile Asp Phe Leu Lys Asp Val Met Glu Ser	
160 165 170	
atg aac aaa gaa gaa atg gag atc aca act cat ttt cag aga aag aga	757
Met Asn Lys Glu Glu Met Glu Ile Thr Thr His Phe Gln Arg Lys Arg	
175 180 185	
cga gtg aga gac aat atg act aag aaa atg gtg aca cag aga aca ata	805
Arg Val Arg Asp Asn Met Thr Lys Lys Met Val Thr Gln Arg Thr Ile	
190 195 200 205	
ggg aaa agg aag cag aga ttg aac aaa agg agt tat cta att agg gca	853
Gly Lys Arg Lys Gln Arg Leu Asn Lys Arg Ser Tyr Leu Ile Arg Ala	
210 215 220	
tta acc ctg aac aca atg acc aaa gat gct gag aga ggg aag cta aaa	901
Leu Thr Leu Asn Thr Met Thr Lys Asp Ala Glu Arg Gly Lys Leu Lys	
225 230 235	
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Arg Arg Ala Ile Ala Thr Pro Gly Met Gln Ile Arg Gly Phe Val Tyr	
240 245 250	
ttt gtt gag aca ctg gcg aga agc att tgc gag aag ctt gaa cag tct	997
Phe Val Glu Thr Leu Ala Arg Ser Ile Cys Glu Lys Leu Glu Gln Ser	
255 260 265	
ggg cta cca gtt gga ggg aat gag aag aaa gct aaa ttg gca aat gtc	1045
Gly Leu Pro Val Gly Gly Asn Glu Lys Lys Ala Lys Leu Ala Asn Val	
270 275 280 285	
gtg agg aag atg atg acg aac tca caa gac act gag ctc tct ttc aca	1093
Val Arg Lys Met Met Thr Asn Ser Gln Asp Thr Glu Leu Ser Phe Thr	
290 295 300	

atc acc gga gac aat acc aaa tgg aat gag aac caa aac ccc cga atg Ile Thr Gly Asp Asn Thr Lys Trp Asn Glu Asn Gln Asn Pro Arg Met 305 310 315	1141
ttc ctg gca atg ata aca tac atc aca aga aac caa cct gag tgg ttt Phe Leu Ala Met Ile Thr Tyr Ile Thr Arg Asn Gln Pro Glu Trp Phe 320 325 330	1189
aga aat gtc ttg agc atc gcg ccg ata atg ttt tcg aac aaa atg gcg Arg Asn Val Leu Ser Ile Ala Pro Ile Met Phe Ser Asn Lys Met Ala 335 340 345	1237
agg cta ggg aaa ggg tac atg ttc gaa agc aaa agc atg aag ctc cga Arg Leu Gly Lys Gly Tyr Met Phe Glu Ser Lys Ser Met Lys Leu Arg 350 355 360 365	1285
aca caa ata cca gca gaa atg cta gca agt att gat cta aaa tat ttc Thr Gln Ile Pro Ala Glu Met Leu Ala Ser Ile Asp Leu Lys Tyr Phe 370 375 380	1333
aat gaa cca aca agg aag aaa atc gag aaa ata agg cct ctc ata ata Asn Glu Pro Thr Arg Lys Lys Ile Glu Lys Ile Arg Pro Leu Ile Ile 385 390 395	1381
gac ggc aca gcc tca tta agc ccg gga atg atg atg ggt atg ttc aac Asp Gly Thr Ala Ser Leu Ser Pro Gly Met Met Met Gly Met Phe Asn 400 405 410	1429
atg ctg agt aca gtg ttg gga gtc tca atc ctg aat ctt ggg caa aag Met Leu Ser Thr Val Leu Gly Val Ser Ile Leu Asn Leu Gly Gln Lys 415 420 425	1477
aga tac acc aaa acc aca tac tgg tgg gat gga ctt cag tcc tct gat Arg Tyr Thr Lys Thr Tyr Trp Trp Asp Gly Leu Gln Ser Ser Asp 430 435 440 445	1525
gat ttt gct ctc atc gtg aat gca cca aat cat gag gga ata caa gcg Asp Phe Ala Leu Ile Val Asn Ala Pro Asn His Glu Gly Ile Gln Ala 450 455 460	1573
gga gtg gat aga ttc tac aga acc tgc aag cta gtt ggg atc aat atg Gly Val Asp Arg Phe Tyr Arg Thr Cys Lys Leu Val Gly Ile Asn Met 465 470 475	1621
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ccc agc ttt ggg gtg tct ggg atc aac gag tct gcg gac atg agt att Pro Ser Phe Gly Val Ser Gly Ile Asn Glu Ser Ala Asp Met Ser Ile 510 515 520 525	1765
gga gtt act gtc atc aaa aac aat atg ata aac aat gat ctt ggt cca Gly Val Thr Val Ile Lys Asn Asn Met Ile Asn Asn Asp Leu Gly Pro 530 535 540	1813
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ctg gtc tcc gac gga ggc cca aat tta tac aac att aga aat ctc cac Leu Val Ser Asp Gly Gly Pro Asn Leu Tyr Asn Ile Arg Asn Leu His 590 595 600 605	2005
att cct gaa gtc tgc ttg aaa tgg gaa ttg atg gat gag gat tac cag Ile Pro Glu Val Cys Leu Lys Trp Glu Leu Met Asp Glu Asp Tyr Gln 610 615 620	2053
ggg cgt tta tgc aac cca ctg aac cca ttt gtc aac cat aaa gac att Gly Arg Ileu Cys Asn Pro Leu Asn Pro Phe Val Asn His Lys Asp Ile 625 630 635	2101
gaa tca gtg aac aat gca gtg ata atg cca gca cat ggt cca gcc aaa Glu Ser Val Asn Asn Ala Val Ile Met Pro Ala His Gly Pro Ala Lys 640 645 650	2149
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gaa caa atg tac caa aag tgc tgc aac tta ttt gaa aaa ttc ttc ccc Glu Gln Met Tyr Gln Lys Cys Cys Asn Leu Phe Glu Lys Phe Phe Pro 690 695 700	2293
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agg ata aag aaa gag gag ttc act gag atc atg aag atc tgt tcc acc Arg Ile Lys Lys Glu Glu Phe Thr Glu Ile Met Lys Ile Cys Ser Thr 735 740 745	2437
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 gtttcacttc tggatgcctggc atggggtcag gtgggaccac cgctactg ccggcaggca 5071

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<211> 757

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: pHL3131

<400> 33

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Gly Thr Gly Thr Gly Tyr Thr Met Asp Thr Val Asn Arg Thr His Gln
 35 40 45

Tyr Ser Glu Arg Gly Arg Trp Thr Thr Asn Thr Glu Thr Gly Ala Pro
 50 55 60

Gln Leu Asn Pro Ile Asp Gly Pro Leu Pro Glu Asp Asn Glu Pro Ser
 65 70 75 80

Gly Tyr Ala Gln Thr Asp Cys Val Leu Glu Ala Met Ala Phe Leu Glu
 85 90 95

Glu Ser His Pro Gly Ile Phe Glu Thr Ser Cys Leu Glu Thr Met Glu
 100 105 110

Val Val Gln Gln Thr Arg Val Asp Lys Leu Thr Gln Gly Arg Gln Thr
 115 120 125

Tyr Asp Trp Thr Leu Asn Arg Asn Gln Pro Ala Ala Thr Ala Leu Ala
 130 135 140

Asn Thr Ile Glu Val Phe Arg Ser Asn Gly Leu Thr Ala Asn Glu Ser
 145 150 155 160

Gly Arg Leu Ile Asp Phe Leu Lys Asp Val Met Glu Ser Met Asn Lys
 165 170 175

Glu Glu Met Glu Ile Thr Thr His Phe Gln Arg Lys Arg Arg Val Arg
 180 185 190

Asp Asn Met Thr Lys Lys Met Val Thr Gln Arg Thr Ile Gly Lys Arg
 195 200 205

Lys Gln Arg Leu Asn Lys Arg Ser Tyr Leu Ile Arg Ala Leu Thr Leu
 210 215 220

Asn Thr Met Thr Lys Asp Ala Glu Arg Gly Lys Leu Lys Arg Arg Ala
 225 230 235 240

Ile Ala Thr Pro Gly Met Gln Ile Arg Gly Phe Val Tyr Phe Val Glu
 245 250 255

Thr Leu Ala Arg Ser Ile Cys Glu Lys Leu Glu Gln Ser Gly Leu Pro
 260 265 270

Val Gly Gly Asn Glu Lys Lys Ala Lys Leu Ala Asn Val Val Arg Lys
 275 280 285

Met Met Thr Asn Ser Gln Asp Thr Glu Leu Ser Phe Thr Ile Thr Gly
 290 295 300
 Asp Asn Thr Lys Trp Asn Glu Asn Gln Asn Pro Arg Met Phe Leu Ala
 305 310 315 320
 Met Ile Thr Tyr Ile Thr Arg Asn Gln Pro Glu Trp Phe Arg Asn Val
 325 330 335
 Leu Ser Ile Ala Pro Ile Met Phe Ser Asn Lys Met Ala Arg Leu Gly
 340 345 350
 Lys Gly Tyr Met Phe Glu Ser Lys Ser Met Lys Leu Arg Thr Gln Ile
 355 360 365
 Pro Ala Glu Met Leu Ala Ser Ile Asp Leu Lys Tyr Phe Asn Glu Pro
 370 375 380
 Thr Arg Lys Lys Ile Glu Lys Ile Arg Pro Leu Ile Ile Asp Gly Thr
 385 390 395 400
 Ala Ser Leu Ser Pro Gly Met Met Met Gly Met Phe Asn Met Leu Ser
 405 410 415
 Thr Val Leu Gly Val Ser Ile Leu Asn Leu Gly Gln Lys Arg Tyr Thr
 420 425 430
 Lys Thr Thr Tyr Trp Trp Asp Gly Leu Gln Ser Ser Asp Asp Phe Ala
 435 440 445
 Leu Ile Val Asn Ala Pro Asn His Glu Gly Ile Gln Ala Gly Val Asp
 450 455 460
 Arg Phe Tyr Arg Thr Cys Lys Leu Val Gly Ile Asn Met Ser Lys Lys
 465 470 475 480
 Lys Ser Tyr Ile Asn Arg Thr Gly Thr Phe Glu Phe Thr Ser Phe Phe
 485 490 495
 Tyr Arg Tyr Gly Phe Val Ala Asn Phe Ser Met Glu Leu Pro Ser Phe
 500 505 510
 Gly Val Ser Gly Ile Asn Glu Ser Ala Asp Met Ser Ile Gly Val Thr
 515 520 525
 Val Ile Lys Asn Asn Met Ile Asn Asn Asp Leu Gly Pro Ala Thr Ala
 530 535 540
 Gln Met Ala Leu Gln Leu Phe Ile Lys Asp Tyr Arg Tyr Thr Tyr Arg
 545 550 555 560
 Cys His Arg Gly Asp Thr Gln Ile Gln Thr Arg Arg Ser Phe Glu Ile
 565 570 575
 Lys Lys Leu Trp Glu Gln Thr His Ser Lys Ala Gly Leu Leu Val Ser
 580 585 590
 Asp Gly Gly Pro Asn Leu Tyr Asn Ile Arg Asn Leu His Ile Pro Glu
 595 600 605
 Val Cys Leu Lys Trp Glu Leu Met Asp Glu Asp Tyr Gln Gly Arg Leu
 610 615 620
 Cys Asn Pro Leu Asn Pro Phe Val Asn His Lys Asp Ile Glu Ser Val
 625 630 635 640

Asn Asn Ala Val Ile Met Pro Ala His Gly Pro Ala Lys Asn Met Glu
 645 650 655

Tyr Asp Ala Val Ala Thr Thr His Ser Trp Ile Pro Lys Arg Asn Arg
 660 665 670

Ser Ile Leu Asn Thr Ser Gln Arg Gly Ile Leu Glu Asp Glu Gln Met
 675 680 685

Tyr Gln Lys Cys Cys Asn Leu Phe Glu Lys Phe Phe Pro Ser Ser Ser
 690 695 700

Tyr Arg Arg Pro Val Gly Ile Ser Ser Met Val Glu Ala Met Val Ser
 705 710 715 720

Arg Ala Arg Ile Asp Ala Arg Ile Asp Phe Glu Ser Gly Arg Ile Lys
 725 730 735

Lys Glu Glu Phe Thr Glu Ile Met Lys Ile Cys Ser Thr Ile Glu Glu
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Leu Arg Arg Gln Lys
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<210> 34

<211> 5169

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: pHL3203

<220>

<221> CDS

<222> (191)..(2461)

<400> 34

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acaaagtgtc gcccggagta ctggtcgacc tccgaagttg ggggggagcg aaagcaggca 180

aaccatttga atg gat gtc aat ccg act tta ctt ttc tta aaa gtg cca 229
 Met Asp Val Asn Pro Thr Leu Leu Phe Leu Lys Val Pro

1 5 10

gca caa aat gct ata agc aca act ttc cct tat act gga gac cct cct 277
 Ala Gln Asn Ala Ile Ser Thr Thr Phe Pro Tyr Thr Gly Asp Pro Pro
 15 20 25

tac agc cat ggg aca gga aca gga tac acc atg gat act gtc aac agg 325
 Tyr Ser His Gly Thr Gly Thr Gly Tyr Thr Met Asp Thr Val Asn Arg
 30 35 40 45

aca cat cag tac tca gaa agg gga aga tgg aca aca aac acc gaa act 373
 Thr His Gln Tyr Ser Glu Arg Gly Arg Trp Thr Thr Asn Thr Glu Thr
 50 55 60

gga gca ccg caa ctc aac ccg att gat ggg cca ctg cca gaa gac aat 421
 Gly Ala Pro Gln Leu Asn Pro Ile Asp Gly Pro Leu Pro Glu Asp Asn
 65 70 75

gaa cca agt ggt tat gcc caa aca gat tgt gta ttg gaa gca atg gcc 469
 Glu Pro Ser Gly Tyr Ala Gln Thr Asp Cys Val Leu Glu Ala Met Ala
 80 85 90

ttc ctt gag gaa tcc cat cct ggt atc ttt gag acc tcg tgt ctt gaa	517
Phe Leu Glu Glu Ser His Pro Gly Ile Phe Glu Thr Ser Cys Leu Glu	
95 100 105	
acg atg qag gtt gtt cag caa aca cga gtg gac aag ctg aca caa ggc	565
Thr Met Glu Val Val Gln Gln Thr Arg Val Asp Lys Leu Thr Gln Gly	
110 115 120 125	
cga cag acc tat gac tgg act cta aat agg aac cag cct gct gca aca	613
Arg Gln Thr Tyr Asp Trp Thr Leu Asn Arg Asn Gln Pro Ala Ala Thr	
130 135 140	
gca ttg gcc aac aca ata gaa gtg ttc aca aat ggc ctc acg gcc	661
Ala Leu Ala Asn Thr Ile Glu Val Phe Arg Ser Asn Gly Leu Thr Ala	
145 150 155	
aat gaa tct gga agg ctc ata gac ttc ctt aag gat gta atg gag tca	709
Asn Glu Ser Gly Arg Leu Ile Asp Phe Leu Lys Asp Val Met Glu Ser	
160 165 170	
atg aac aaa gaa gaa atg gag atc aca act cat ttt cag aga aag aga	757
Met Asn Lys Glu Glu Met Glu Ile Thr Thr His Phe Gln Arg Lys Arg	
175 180 185	
cga gtg aga gac aat atg act aag aaa atg gtg aca cag aga aca ata	805
Arg Val Arg Asp Asn Met Thr Lys Lys Met Val Thr Gln Arg Thr Ile	
190 195 200 205	
ggt aaa agg aag cag aga ttg aac aaa agg agt tat cta att agg gca	853
Gly Lys Arg Lys Gln Arg Leu Asn Lys Arg Ser Tyr Leu Ile Arg Ala	
210 215 220	
tta acc ctg aac aca atg acc aaa gat gct gag aga ggg aag cta aaa	901
Leu Thr Leu Asn Thr Met Thr Lys Asp Ala Glu Arg Gly Lys Leu Lys	
225 230 235	
cgg aga gca att gca acc cca ggg atg caa ata agg ggg ttt gta tac	949
Arg Arg Ala Ile Ala Thr Pro Gly Met Gln Ile Arg Gly Phe Val Tyr	
240 245 250	
ttt gtt gag aca cta gca agg agt ata tgt gag aaa ctt gaa caa tca	997
Phe Val Glu Thr Leu Ala Arg Ser Ile Cys Glu Lys Leu Glu Gln Ser	
255 260 265	
gga ttg cca gtt gga ggc aat gag aag aaa gca aag ttg gca aat gtt	1045
Gly Leu Pro Val Gly Gly Asn Glu Lys Lys Ala Lys Leu Ala Asn Val	
270 275 280 285	
gta agg aag atg atg acc aat tct cag gac act gaa att tct ttc acc	1093
Val Arg Lys Met Met Thr Asn Ser Gln Asp Thr Glu Ile Ser Phe Thr	
290 295 300	
atc act gga gat aac acc aaa tgg aac gaa aat cag aac cct cggt atg	1141
Ile Thr Gly Asp Asn Thr Lys Trp Asn Glu Asn Gln Asn Pro Arg Met	
305 310 315	
ttt ttg gcc atg atc aca tat ata acc aga aat cag ccc gaa tgg ttc	1189
Phe Leu Ala Met Ile Thr Tyr Ile Thr Arg Asn Gln Pro Glu Trp Phe	
320 325 330	
aga aat gtt cta agt att gct cca ata atg ttc tca aac aaa atg gcg	1237
Arg Asn Val Leu Ser Ile Ala Pro Ile Met Phe Ser Asn Lys Met Ala	
335 340 345	

aga ctg gga aag ggg tac atg ttt gag agc aag agt atg aaa att aga		1285
Arg Leu Gly Lys Gly Tyr Met Phe Glu Ser Lys Ser Met Lys Ile Arg		
350 355 360 365		
act caa ata cct gca gaa atg cta gca agc atc gat ttg aaa tac ttc		1333
Thr Gln Ile Pro Ala Glu Met Leu Ala Ser Ile Asp Leu Lys Tyr Phe		
370 375 380		
aat gat tca act aga aag aag att gaa aaa atc cgg cgg ctc tta ata		1381
Asn Asp Ser Thr Arg Lys Lys Ile Glu Lys Ile Arg Pro Leu Leu Ile		
385 390 395		
gat ggg act gca tca ttg agc cct gga atg atg atg ggc atg ttc aat		1429
Asp Gly Thr Ala Ser Leu Ser Pro Gly Met Met Met Gly Met Phe Asn		
400 405 410		
atg tta agt act gta tta ggc gtc tcc atc ctg aat ctt gga caa aag		1477
Met Leu Ser Thr Val Leu Gly Val Ser Ile Leu Asn Leu Gly Gln Lys		
415 420 425		
aga cac acc aag act act tac tgg tgg gat ggt ctt caa tct tct gat		1525
Arg His Thr Lys Thr Tyr Trp Trp Asp Gly Leu Gln Ser Ser Asp		
430 435 440 445		
gat ttt gct ctg att gtg aat gca ccc aat cat gaa ggg att caa gcc		1573
Asp Phe Ala Leu Ile Val Asn Ala Pro Asn His Glu Gly Ile Gln Ala		
450 455 460		
gga gtc aac agg ttt tat cga acc tgt aag cta ctt gga att aat atg		1621
Gly Val Asn Arg Phe Tyr Arg Thr Cys Lys Leu Leu Gly Ile Asn Met		
465 470 475		
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Ser Lys Lys Ser Tyr Ile Asn Arg Thr Gly Thr Phe Glu Phe Thr		
480 485 490		
agc ttt ttc tat cgt tat ggg ttt gtt gcc aat ttc agc atg gag ctt		1717
Ser Phe Phe Tyr Arg Tyr Gly Phe Val Ala Asn Phe Ser Met Glu Leu		
495 500 505		
ccc agc ttt ggg gtg tct ggg atc aac gag tct gcg gac atg agt att		1765
Pro Ser Phe Gly Val Ser Gly Ile Asn Glu Ser Ala Asp Met Ser Ile		
510 515 520 525		
gga gtt act gtc atc aaa aac aat atg ata aac aat gat ctt ggt cca		1813
Gly Val Thr Val Ile Lys Asn Asn Met Ile Asn Asn Asp Leu Gly Pro		
530 535 540		
gca acc gct caa atg gcc ctt cag ctg ttc atc aaa gat tac agg tac		1861
Ala Thr Ala Gln Met Ala Leu Gln Leu Phe Ile Lys Asp Tyr Arg Tyr		
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Thr Tyr Arg Cys His Arg Gly Asp Thr Gln Ile Gln Thr Arg Arg Ser		
560 565 570		
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Phe Glu Ile Lys Lys Leu Trp Glu Gln Thr His Ser Lys Ala Gly Leu		
575 580 585		
ctg gtc tcc gac gga ggc cca aat ttg tac aac att cgg aat ctc cac		2005
Leu Val Ser Asp Gly Gly Pro Asn Leu Tyr Asn Ile Arg Asn Leu His		
590 595 600 605		
atc ccg gaa gtt tgc ctg aaa tgg gaa cta atg gat gaa gac tat cag		2053
Ile Pro Glu Val Cys Leu Lys Trp Glu Leu Met Asp Glu Asp Tyr Gln		
610 615 620		

gga aga ctt tgt aat ccc atg aac ccg ttt gtc agt cat aag gaa att	2101		
Gly Arg Leu Cys Asn Pro Met Asn Pro Phe Val Ser His Lys Glu Ile			
625	630	635	
gaa tct gta aac aat gct gcg gta atg cca gcc cat ggt cca gcc aaa	2149		
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640	645	650	
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Ser Met Glu Tyr Asp Ala Val Ala Thr Thr His Ser Trp Ile Pro Lys			
655	660	665	
aga aac cgt tcc att ctc aat acg agt caa agg gga atc ctt gag gat	2245		
Arg Asn Arg Ser Ile Leu Asn Thr Ser Gln Arg Gly Ile Leu Glu Asp			
670	675	680	685
gaa caa atg tac cag aag tgt tgc aac cta ttc gag aaa ttc ttc cct	2293		
Glu Gln Met Tyr Gln Lys Cys Cys Asn Leu Phe Glu Lys Phe Phe Pro			
690	695	700	
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Ser Ser Ser Tyr Arg Arg Pro Val Gly Ile Ser Ser Met Val Glu Ala			
705	710	715	
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Met Val Ser Arg Ala Arg Ile Asp Ala Arg Ile Asp Phe Glu Ser Gly			
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Arg Ile Lys Lys Glu Glu Phe Ala Glu Ile Met Lys Ile Cys Ser Thr			
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Ile Glu Glu Leu Arg Arg Gln Lys			
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<211> 757

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: pHL3203

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 Gly Thr Gly Thr Gly Tyr Thr Met Asp Thr Val Asn Arg Thr His Gln
 35 40 45
 Tyr Ser Glu Arg Gly Arg Trp Thr Thr Asn Thr Glu Thr Gly Ala Pro
 50 55 60
 Gln Leu Asn Pro Ile Asp Gly Pro Leu Pro Glu Asp Asn Glu Pro Ser
 65 70 75 80
 Gly Tyr Ala Gln Thr Asp Cys Val Leu Glu Ala Met Ala Phe Leu Glu
 85 90 95
 Glu Ser His Pro Gly Ile Phe Glu Thr Ser Cys Leu Glu Thr Met Glu
 100 105 110
 Val Val Gln Gln Thr Arg Val Asp Lys Leu Thr Gln Gly Arg Gln Thr
 115 120 125
 Tyr Asp Trp Thr Leu Asn Arg Asn Gln Pro Ala Ala Thr Ala Leu Ala
 130 135 140
 Asn Thr Ile Glu Val Phe Arg Ser Asn Gly Leu Thr Ala Asn Glu Ser
 145 150 155 160
 Gly Arg Leu Ile Asp Phe Leu Lys Asp Val Met Glu Ser Met Asn Lys
 165 170 175
 Glu Glu Met Glu Ile Thr Thr His Phe Gln Arg Lys Arg Arg Val Arg
 180 185 190
 Asp Asn Met Thr Lys Lys Met Val Thr Gln Arg Thr Ile Gly Lys Arg
 195 200 205
 Lys Gln Arg Leu Asn Lys Arg Ser Tyr Leu Ile Arg Ala Leu Thr Leu
 210 215 220
 Asn Thr Met Thr Lys Asp Ala Glu Arg Gly Lys Leu Lys Arg Arg Ala
 225 230 235 240
 Ile Ala Thr Pro Gly Met Gln Ile Arg Gly Phe Val Tyr Phe Val Glu
 245 250 255
 Thr Leu Ala Arg Ser Ile Cys Glu Lys Leu Glu Gln Ser Gly Leu Pro
 260 265 270
 Val Gly Gly Asn Glu Lys Lys Ala Lys Leu Ala Asn Val Val Arg Lys
 275 280 285
 Met Met Thr Asn Ser Gln Asp Thr Glu Ile Ser Phe Thr Ile Thr Gly
 290 295 300
 Asp Asn Thr Lys Trp Asn Glu Asn Gln Asn Pro Arg Met Phe Leu Ala
 305 310 315 320
 Met Ile Thr Tyr Ile Thr Arg Asn Gln Pro Glu Trp Phe Arg Asn Val
 325 330 335
 Leu Ser Ile Ala Pro Ile Met Phe Ser Asn Lys Met Ala Arg Leu Gly
 340 345 350

Lys Gly Tyr Met Phe Glu Ser Lys Ser Met Lys Ile Arg Thr Gln Ile
 355 360 365
 Pro Ala Glu Met Leu Ala Ser Ile Asp Leu Lys Tyr Phe Asn Asp Ser
 370 375 380
 Thr Arg Lys Lys Ile Glu Lys Ile Arg Pro Leu Leu Ile Asp Gly Thr
 385 390 395 400
 Ala Ser Leu Ser Pro Gly Met Met Gly Met Phe Asn Met Leu Ser
 405 410 415
 Thr Val Leu Gly Val Ser Ile Leu Asn Leu Gly Gln Lys Arg His Thr
 420 425 430
 Lys Thr Thr Tyr Trp Trp Asp Gly Leu Gln Ser Ser Asp Asp Phe Ala
 435 440 445
 Leu Ile Val Asn Ala Pro Asn His Glu Gly Ile Gln Ala Gly Val Asn
 450 455 460
 Arg Phe Tyr Arg Thr Cys Lys Leu Leu Gly Ile Asn Met Ser Lys Lys
 465 470 475 480
 Lys Ser Tyr Ile Asn Arg Thr Gly Thr Phe Glu Phe Thr Ser Phe Phe
 485 490 495
 Tyr Arg Tyr Gly Phe Val Ala Asn Phe Ser Met Glu Leu Pro Ser Phe
 500 505 510
 Gly Val Ser Gly Ile Asn Glu Ser Ala Asp Met Ser Ile Gly Val Thr
 515 520 525
 Val Ile Lys Asn Asn Met Ile Asn Asn Asp Leu Gly Pro Ala Thr Ala
 530 535 540
 Gln Met Ala Leu Gln Leu Phe Ile Lys Asp Tyr Arg Tyr Thr Tyr Arg
 545 550 555 560
 Cys His Arg Gly Asp Thr Gln Ile Gln Thr Arg Arg Ser Phe Glu Ile
 565 570 575
 Lys Lys Leu Trp Glu Gln Thr His Ser Lys Ala Gly Leu Leu Val Ser
 580 585 590
 Asp Gly Gly Pro Asn Leu Tyr Asn Ile Arg Asn Leu His Ile Pro Glu
 595 600 605
 Val Cys Leu Lys Trp Glu Leu Met Asp Glu Asp Tyr Gln Gly Arg Leu
 610 615 620
 Cys Asn Pro Met Asn Pro Phe Val Ser His Lys Glu Ile Glu Ser Val
 625 630 635 640
 Asn Asn Ala Ala Val Met Pro Ala His Gly Pro Ala Lys Ser Met Glu
 645 650 655
 Tyr Asp Ala Val Ala Thr Thr His Ser Trp Ile Pro Lys Arg Asn Arg
 660 665 670
 Ser Ile Leu Asn Thr Ser Gln Arg Gly Ile Leu Glu Asp Glu Gln Met
 675 680 685
 Tyr Gln Lys Cys Cys Asn Leu Phe Glu Lys Phe Phe Pro Ser Ser Ser
 690 695 700

Tyr Arg Arg Pro Val Gly Ile Ser Ser Met Val Glu Ala Met Val Ser
 705 710 715 720

Arg Ala Arg Ile Asp Ala Arg Ile Asp Phe Glu Ser Gly Arg Ile Lys
 725 730 735

Lys Glu Glu Phe Ala Glu Ile Met Lys Ile Cys Ser Thr Ile Glu Glu
 740 745 750

Leu Arg Arg Gln Lys
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<210> 36

<211> 5169

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: pHL3204

<220>

<221> CDS

<222> (191)..(2461)

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acaaagtgtc gcccggagta ctggtcgacc tccgaagttg ggggggagcgc aaagcaggca 180

aaccatttga atg gat gtc aat ccg act tta ctt ttc tta aaa gtg cca 229
 Met Asp Val Asn Pro Thr Leu Leu Phe Leu Lys Val Pro
 1 5 10

gca caa aat gct ata agc aca act ttc cct tat act gga gac cct cct 277
 Ala Gln Asn Ala Ile Ser Thr Thr Phe Pro Tyr Thr Gly Asp Pro Pro
 15 20 25

tac agc cat ggg aca gga aca gga tac acc atg gat act gtc aac agg 325
 Tyr Ser His Gly Thr Gly Thr Gly Tyr Thr Met Asp Thr Val Asn Arg
 30 35 40 45

aca cat cag tac tca gaa agg gga aga tgg aca aca aac acc gaa act 373
 Thr His Gln Tyr Ser Glu Arg Gly Arg Trp Thr Thr Asn Thr Glu Thr
 50 55 60

gga gca ccg caa ctc aac ccg att gat ggg cca ctg cca gaa gac aat 421
 Gly Ala Pro Gln Leu Asn Pro Ile Asp Gly Pro Leu Pro Glu Asp Asn
 65 70 75

gaa cca agt ggt tat gcc caa aca gat tgt gta ttg gaa gca atg gcc 469
 Glu Pro Ser Gly Tyr Ala Gln Thr Asp Cys Val Leu Glu Ala Met Ala
 80 85 90

ttc ctt gag gaa tcc cat cct ggt atc ttt gag acc tcg tgt ctt gaa 517
 Phe Leu Glu Glu Ser His Pro Gly Ile Phe Glu Thr Ser Cys Leu Glu
 95 100 105

acg atg gag gtt gtt cag caa aca cga gtg gac aag ctg aca caa ggc 565
 Thr Met Glu Val Val Gln Gln Thr Arg Val Asp Lys Leu Thr Gln Gly
 110 115 120 125

cga cag acc tat gac tgg act cta aat agg aac cag cct gct gca aca 613
 Arg Gln Thr Tyr Asp Trp Thr Leu Asn Arg Asn Gln Pro Ala Ala Thr
 130 135 140

gca ttg gcc aac aca ata gaa gtg ttc aga tca aat ggc ctc acg gcc Ala Leu Ala Asn Thr Ile Glu Val Phe Arg Ser Asn Gly Leu Thr Ala 145 150 155	661
aat gaa tct gga agg ctc ata gac ttc ctt aag gat gta atg gag tca Asn Glu Ser Gly Arg Leu Ile Asp Phe Leu Lys Asp Val Met Glu Ser 160 165 170	709
atg aac aaa gaa gaa atg gag atc aca act cat ttt cag aga aag aga Met Asn Lys Glu Met Glu Ile Thr Thr His Phe Gln Arg Lys Arg 175 180 185	757
cga gtg aga gac aat atg act aag aaa atg gtg aca cag aga aca ata Arg Val Arg Asp Asn Met Thr Lys Lys Met Val Thr Gln Arg Thr Ile 190 195 200 205	805
ggg aaa agg aag cag aga ttg aac aaa agg agt tat cta att agg gca Gly Lys Arg Lys Gln Arg Leu Asn Lys Arg Ser Tyr Leu Ile Arg Ala 210 215 220	853
tta acc ctg aac aca atg acc aaa gat gct gag aga ggg aag cta aaa Leu Thr Leu Asn Thr Met Thr Lys Asp Ala Glu Arg Gly Lys Leu Lys 225 230 235	901
cgg aga gca att gca acc cca ggg atg caa ata agg ggg ttt gta tac Arg Arg Ala Ile Ala Thr Pro Gly Met Gln Ile Arg Gly Phe Val Tyr 240 245 250	949
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gta agg aag atg atg acc aat tct cag gac act gaa att tct ttc acc Val Arg Lys Met Met Thr Asn Ser Gln Asp Thr Glu Ile Ser Phe Thr 290 295 300	1093
atc act gga gat aac acc aaa tgg aac gaa aat cag aac cct cgg atg Ile Thr Gly Asp Asn Thr Lys Trp Asn Glu Asn Gln Asn Pro Arg Met 305 310 315	1141
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aga aat gtt cta agt att gct cca ata atg ttc tca aac aaa atg gcg Arg Asn Val Leu Ser Ile Ala Pro Ile Met Phe Ser Asn Lys Met Ala 335 340 345	1237
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aat gat tca act aga aag aag att gaa aaa atc cgg ccg ctc tta ata Asn Asp Ser Thr Arg Lys Lys Ile Glu Lys Ile Arg Pro Leu Leu Ile 385 390 395	1381

gat ggg act gca tca ttg agc cct gga atg atg atg ggc atg ttc aat		1429
Asp Gly Thr Ala Ser Leu Ser Pro Gly Met Met Met Gly Met Phe Asn		
400	405	410
atg tta agt act gta tta ggc gtc tcc atc ctg aat ctt gga caa aag		1477
Met Leu Ser Thr Val Leu Gly Val Ser Ile Leu Asn Leu Gly Gln Lys		
415	420	425
aga cac acc aag act act tac tgg tgg gat ggt ctt caa tct tct gat		1525
Arg His Thr Lys Thr Tyr Trp Trp Asp Gly Leu Gln Ser Ser Asp		
430	435	440
445		
gat ttt gct ctg att gtg aat gca ccc aat cat gaa ggg att caa gcc		1573
Asp Phe Ala Leu Ile Val Asn Ala Pro Asn His Glu Gly Ile Gln Ala		
450	455	460
gga gtc aac agg ttt tat cga acc tgg aag cta ctt gga att aat atg		1621
Gly Val Asn Arg Phe Tyr Arg Thr Cys Lys Leu Leu Gly Ile Asn Met		
465	470	475
agc aag aaa aag tct tac ata aac aga aca ggt aca ttt gaa ttc aca		1669
Ser Lys Lys Ser Tyr Ile Asn Arg Thr Gly Thr Phe Glu Phe Thr		
480	485	490
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Ser Phe Phe Tyr Arg Tyr Gly Phe Val Ala Asn Phe Ser Met Glu Leu		
495	500	505
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Pro Ser Phe Gly Val Ser Gly Ile Asn Glu Ser Ala Asp Met Ser Ile		
510	515	520
525		
gga gta aca gtg ata aag aat aac atg ata aac aat gat ctt gga ccg		1813
Gly Val Thr Val Ile Lys Asn Asn Met Ile Asn Asn Asp Leu Gly Pro		
530	535	540
gca aca gcc caa atg gct ctc caa tta ttc atc aag gac tac aga tat		1861
Ala Thr Ala Gln Met Ala Leu Gln Leu Phe Ile Lys Asp Tyr Arg Tyr		
545	550	555
aca tac agg tgt cac agg gga gac aca caa atc caa acg agg agg tca		1909
Thr Tyr Arg Cys His Arg Gly Asp Thr Gln Ile Gln Thr Arg Arg Ser		
560	565	570
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Phe Glu Leu Lys Lys Leu Trp Glu Gln Thr Arg Ser Lys Ala Gly Leu		
575	580	585
ttg gtt tca gat ggc gga cca aac ctg tac aac att aga aat ctc cac		2005
Leu Val Ser Asp Gly Gly Pro Asn Leu Tyr Asn Ile Arg Asn Leu His		
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605		
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Ile Pro Glu Val Cys Leu Lys Trp Glu Leu Met Asp Glu Asp Tyr Gln		
610	615	620
ggg cgt tta tgc aac cca ctg aac cca ttt gtc aac cat aaa gac att		2101
Gly Arg Leu Cys Asn Pro Leu Asn Pro Phe Val Asn His Lys Asp Ile		
625	630	635
gaa tca gtg aac aat gca gtg ata atg cca gca cat ggt cca gcc aaa		2149
Glu Ser Val Asn Asn Ala Val Ile Met Pro Ala His Gly Pro Ala Lys		
640	645	650
655		
aac atg gag tat gat gct gtt gca aca aca cac tcc tgg atc ccc aaa		2197
Asn Met Glu Tyr Asp Ala Val Ala Thr Thr His Ser Trp Ile Pro Lys		
660	665	

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Arg Asn Arg Ser Ile Leu Asn Thr Ser Gln Arg Gly Ile Leu Glu Asp	
670 675 680 685	
gaa caa atg tac caa aag tgc tgc aac tta ttt gaa aaa ttc ttc ccc	2293
Glu Gln Met Tyr Gln Lys Cys Cys Asn Leu Phe Glu Lys Phe Phe Pro	
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Ser Ser Tyr Arg Arg Pro Val Gly Ile Ser Ser Met Val Glu Ala	
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Met Val Ser Arg Ala Arg Ile Asp Ala Arg Ile Asp Phe Glu Ser Gly	
720 725 730	
agg ata aag aaa gag gag ttc act gag atc atg aag atc tgt tcc acc	2437
Arg Ile Lys Lys Glu Glu Phe Thr Glu Ile Met Lys Ile Cys Ser Thr	
735 740 745	
att gaa gag ctc aga cgg caa aaa tagtgaattt agcttgcct tcataaaaaa	2491
Ile Glu Glu Leu Arg Arg Gln Lys	
750 755	
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<211> 757

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: pHL3204

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Gly Thr Gly Thr Gly Tyr Thr Met Asp Thr Val Asn Arg Thr His Gln
 35 40 45

Tyr Ser Glu Arg Gly Arg Trp Thr Thr Asn Thr Glu Thr Gly Ala Pro
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Gln Leu Asn Pro Ile Asp Gly Pro Leu Pro Glu Asp Asn Glu Pro Ser
 65 70 75 80
 Gly Tyr Ala Gln Thr Asp Cys Val Leu Glu Ala Met Ala Phe Leu Glu
 85 90 95
 Glu Ser His Pro Gly Ile Phe Glu Thr Ser Cys Leu Glu Thr Met Glu
 100 105 110
 Val Val Gln Gln Thr Arg Val Asp Lys Leu Thr Gln Gly Arg Gln Thr
 115 120 125
 Tyr Asp Trp Thr Leu Asn Arg Asn Gln Pro Ala Ala Thr Ala Leu Ala
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 Asn Thr Ile Glu Val Phe Arg Ser Asn Gly Leu Thr Ala Asn Glu Ser
 145 150 155 160
 Gly Arg Leu Ile Asp Phe Leu Lys Asp Val Met Glu Ser Met Asn Lys
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 Glu Glu Met Glu Ile Thr Thr His Phe Gln Arg Lys Arg Arg Val Arg
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 Asp Asn Met Thr Lys Lys Met Val Thr Gln Arg Thr Ile Gly Lys Arg
 195 200 205
 Lys Gln Arg Leu Asn Lys Arg Ser Tyr Leu Ile Arg Ala Leu Thr Leu
 210 215 220
 Asn Thr Met Thr Lys Asp Ala Glu Arg Gly Lys Leu Lys Arg Arg Ala
 225 230 235 240
 Ile Ala Thr Pro Gly Met Gln Ile Arg Gly Phe Val Tyr Phe Val Glu
 245 250 255
 Thr Leu Ala Arg Ser Ile Cys Glu Lys Leu Glu Gln Ser Gly Leu Pro
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 Val Gly Gly Asn Glu Lys Ala Lys Leu Ala Asn Val Val Arg Lys
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 290 295 300
 Asp Asn Thr Lys Trp Asn Glu Asn Gln Asn Pro Arg Met Phe Leu Ala
 305 310 315 320
 Met Ile Thr Tyr Ile Thr Arg Asn Gln Pro Glu Trp Phe Arg Asn Val
 325 330 335
 Leu Ser Ile Ala Pro Ile Met Phe Ser Asn Lys Met Ala Arg Leu Gly
 340 345 350
 Lys Gly Tyr Met Phe Glu Ser Lys Ser Met Lys Ile Arg Thr Gln Ile
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 Pro Ala Glu Met Leu Ala Ser Ile Asp Leu Lys Tyr Phe Asn Asp Ser
 370 375 380
 Thr Arg Lys Lys Ile Glu Lys Ile Arg Pro Leu Leu Ile Asp Gly Thr
 385 390 395 400
 Ala Ser Leu Ser Pro Gly Met Met Gly Met Phe Asn Met Leu Ser
 405 410 415

Thr Val Leu Gly Val Ser Ile Leu Asn Leu Gly Gln Lys Arg His Thr
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 Lys Thr Thr Tyr Trp Trp Asp Gly Leu Gln Ser Ser Asp Asp Phe Ala
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 Leu Ile Val Asn Ala Pro Asn His Glu Gly Ile Gln Ala Gly Val Asn
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 Arg Phe Tyr Arg Thr Cys Lys Leu Leu Gly Ile Asn Met Ser Lys Lys
 465 470 475 480
 Lys Ser Tyr Ile Asn Arg Thr Gly Thr Phe Glu Phe Thr Ser Phe Phe
 485 490 495
 Tyr Arg Tyr Gly Phe Val Ala Asn Phe Ser Met Glu Leu Pro Ser Phe
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 Gly Val Ser Gly Ile Asn Glu Ser Ala Asp Met Ser Ile Gly Val Thr
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 Val Ile Lys Asn Asn Met Ile Asn Asn Asp Leu Gly Pro Ala Thr Ala
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 Gln Met Ala Leu Gln Leu Phe Ile Lys Asp Tyr Arg Tyr Thr Tyr Arg
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 Cys His Arg Gly Asp Thr Gln Ile Gln Thr Arg Arg Ser Phe Glu Leu
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 Lys Lys Leu Trp Glu Gln Thr Arg Ser Lys Ala Gly Leu Leu Val Ser
 580 585 590
 Asp Gly Gly Pro Asn Leu Tyr Asn Ile Arg Asn Leu His Ile Pro Glu
 595 600 605
 Val Cys Leu Lys Trp Glu Leu Met Asp Glu Asp Tyr Gln Gly Arg Leu
 610 615 620
 Cys Asn Pro Leu Asn Pro Phe Val Asn His Lys Asp Ile Glu Ser Val
 625 630 635 640
 Asn Asn Ala Val Ile Met Pro Ala His Gly Pro Ala Lys Asn Met Glu
 645 650 655
 Tyr Asp Ala Val Ala Thr Thr His Ser Trp Ile Pro Lys Arg Asn Arg
 660 665 670
 Ser Ile Leu Asn Thr Ser Gln Arg Gly Ile Leu Glu Asp Glu Gln Met
 675 680 685
 Tyr Gln Lys Cys Cys Asn Leu Phe Glu Lys Phe Phe Pro Ser Ser Ser
 690 695 700
 Tyr Arg Arg Pro Val Gly Ile Ser Ser Met Val Glu Ala Met Val Ser
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 Arg Ala Arg Ile Asp Ala Arg Ile Asp Phe Glu Ser Gly Arg Ile Lys
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 Lys Glu Glu Phe Thr Glu Ile Met Lys Ile Cys Ser Thr Ile Glu Glu
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 Leu Arg Arg Gln Lys
 755

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 <211> 5169
 <212> DNA
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<220>
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 acaaaagtgtc gcccggagta ctggtcgacc tccgaagttg ggggggagcg aaagcaggca 180
 aaccatttga atg gat gtc aat ccg act tta ctt ttc tta aaa gtg cca 229
 Met Asp Val Asn Pro Thr Leu Leu Phe Leu Lys Val Pro
 1 5 10

gca caa aat gct ata agc aca act ttc cct tat act gga gac cct cct 277
 Ala Gln Asn Ala Ile Ser Thr Thr Phe Pro Tyr Thr Gly Asp Pro Pro
 15 20 25

tac agc cat ggg aca gga aca gga tac acc atg gat act gtc aac agg 325
 Tyr Ser His Gly Thr Gly Thr Gly Tyr Thr Met Asp Thr Val Asn Arg
 30 35 40 45

aca cat cag tac tca gaa agg gga aga tgg aca aca aac acc gaa act 373
 Thr His Gln Tyr Ser Glu Arg Gly Arg Trp Thr Asn Thr Glu Thr
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gga gca ccg caa ctc aac ccg att gat ggg cca ctg cca gaa gac aat 421
 Gly Ala Pro Gln Leu Asn Pro Ile Asp Gly Pro Leu Pro Glu Asp Asn
 65 70 75

gaa cca agt ggt tat gcc caa aca gat tgt gta ttg gaa gca atg gcc 469
 Glu Pro Ser Gly Tyr Ala Gln Thr Asp Cys Val Leu Glu Ala Met Ala
 80 85 90

ttc ctt gag gaa tcc cat cct ggt atc ttt gag acc tcg tgt ctt gaa 517
 Phe Leu Glu Glu Ser His Pro Gly Ile Phe Glu Thr Ser Cys Leu Glu
 95 100 105

acg atg gag gtt gtt cag caa aca cga gtg gac aag ctg aca caa ggc 565
 Thr Met Glu Val Val Gln Gln Thr Arg Val Asp Lys Leu Thr Gln Gly
 110 115 120 125

cga cag acc tat gac tgg act cta aat agg aac cag cct gct gca aca 613
 Arg Gln Thr Tyr Asp Trp Thr Leu Asn Arg Asn Gln Pro Ala Ala Thr
 130 135 140

gca ttg gcc aac aca ata gaa gtg ttc aga tca aat ggc ctc acg gcc 661
 Ala Leu Ala Asn Thr Ile Glu Val Phe Arg Ser Asn Gly Leu Thr Ala
 145 150 155

aat gaa tct gga agg ctc ata gac ttc ctt aag gat gta atg gag tca 709
 Asn Glu Ser Gly Arg Leu Ile Asp Phe Leu Lys Asp Val Met Glu Ser
 160 165 170

atg aac aaa gaa gaa atg gag atc aca act cat ttt cag aga aag aga 757
 Met Asn Lys Glu Glu Met Glu Ile Thr Thr His Phe Gln Arg Lys Arg
 175 180 185

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Arg	Val	Arg	Asp	Asn	Met	Thr	Lys	Lys	Met	Val	Thr	Gln	Arg	Thr	Ile	
190					195				200				205			
ggt	aaa	agg	aag	cag	aga	ttg	aac	aaa	agg	agt	tat	ctt	att	agg	gca	853
Gly	Lys	Arg	Lys	Gln	Arg	Leu	Asn	Lys	Arg	Ser	Tyr	Leu	Ile	Arg	Ala	
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tta	acc	ctg	aac	aca	atg	acc	aaa	gat	gct	gag	aga	ggg	aag	ctt	aaa	901
Leu	Thr	Leu	Asn	Thr	Met	Thr	Lys	Asp	Ala	Glu	Arg	Gly	Lys	Leu	Lys	
					225				230				235			
cgg	aga	gca	att	gca	aca	cca	ggg	atg	cag	atc	aga	ggg	ttt	gtg	tac	949
Arg	Arg	Ala	Ile	Ala	Thr	Pro	Gly	Met	Gln	Ile	Arg	Gly	Phe	Val	Tyr	
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Phe	Val	Glu	Thr	Leu	Ala	Arg	Ser	Ile	Cys	Glu	Lys	Leu	Glu	Gln	Ser	
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ggg	cta	cca	gtt	gga	ggg	aat	gag	aag	aaa	gct	aaa	ttg	gca	aat	gtc	1045
Gly	Leu	Pro	Val	Gly	Gly	Asn	Glu	Lys	Lys	Ala	Lys	Leu	Ala	Asn	Val	
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gtg	agg	aag	atg	atg	acg	aac	tca	caa	gac	act	gag	ctc	tct	ttc	aca	1093
Val	Arg	Lys	Met	Met	Thr	Asn	Ser	Gln	Asp	Thr	Glu	Leu	Ser	Phe	Thr	
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atc	acc	gga	gac	aat	acc	aaa	tgg	aat	gag	aac	caa	aac	ccc	cga	atg	1141
Ile	Thr	Gly	Asp	Asn	Thr	Lys	Trp	Asn	Glu	Asn	Gln	Asn	Pro	Arg	Met	
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ttc	ctg	gca	atg	ata	aca	ta	atc	aca	aga	aac	caa	cct	gag	tgg	ttt	1189
Phe	Leu	Ala	Met	Ile	Thr	Tyr	Ile	Thr	Arg	Asn	Gln	Pro	Glu	Trp	Phe	
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aga	aat	gtc	ttg	agc	atc	gcg	ccg	ata	atg	ttt	tcg	aac	aaa	atg	gcg	1237
Arg	Asn	Val	Leu	Ser	Ile	Ala	Pro	Ile	Met	Phe	Ser	Asn	Lys	Met	Ala	
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agg	cta	ggg	aaa	ggg	tac	atg	ttc	gaa	agc	aaa	agc	atg	aag	ctc	cga	1285
Arg	Leu	Gly	Lys	Gly	Tyr	Met	Phe	Glu	Ser	Lys	Ser	Met	Lys	Leu	Arg	
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aca	caa	ata	cca	gca	gaa	atg	cta	gca	agc	atc	gat	ttg	aaa	tac	ttc	1333
Thr	Gln	Ile	Pro	Ala	Glu	Met	Leu	Ala	Ser	Ile	Asp	Leu	Lys	Tyr	Phe	
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aat	aat	tca	act	aga	aag	aag	att	gaa	aaa	atc	ccg	ccg	ctc	tta	ata	1381
Asn	Asp	Ser	Thr	Arg	Lys	Lys	Ile	Glu	Lys	Ile	Arg	Pro	Leu	Leu	Ile	
					385				390				395			
gat	ggg	act	gca	tca	ttg	agc	cct	gga	atg	atg	atg	ggc	atg	ttc	aat	1429
Asp	Gly	Thr	Ala	Ser	Leu	Ser	Pro	Gly	Met	Met	Met	Gly	Met	Phe	Asn	
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atg	tta	agt	act	gta	tta	ggc	gtc	tcc	atc	ctg	aat	ctt	gga	caa	aag	1477
Met	Leu	Ser	Thr	Val	Leu	Gly	Val	Ser	Ile	Leu	Asn	Leu	Gly	Gln	Lys	
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aga	cac	acc	aag	act	act	tac	tgg	tgg	gat	ggt	ctt	caa	tct	tct	gat	1525
Arg	His	Thr	Lys	Thr	Thr	Tyr	Trp	Trp	Asp	Gly	Leu	Gln	Ser	Ser	Asp	
					430				435				440		445	
gat	ttt	gct	ctg	att	gtg	aat	gca	ccc	aat	cat	gaa	ggg	att	caa	gcc	1573
Asp	Phe	Ala	Leu	Ile	Val	Asn	Ala	Pro	Asn	His	Glu	Gly	Ile	Gln	Ala	
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att cct gaa gtc tgc ttg aaa tgg gaa tta atg gat gag gat tac cag Ile Pro Glu Val Cys Leu Lys Trp Glu Leu Met Asp Glu Asp Tyr Gln 610 615 620	2053
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 720 725 730

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 Arg Ile Lys Lys Glu Glu Phe Thr Glu Ile Met Lys Ile Cys Ser Thr
 735 740 745

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 Ile Glu Glu Leu Arg Arg Gln Lys
 750 755

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 cgacaaacaa cagataaaac gaaaggccca gtcttcgac tgagccttc gtttatttg 4951
 atgcctggca gttccctact ctcgcattgg gagacccac actaccatcg gcgctacggc 5011
 gtttcacttc tgagttcggc atggggtcag gtgggaccac cgcgctactg ccgcccaggca 5071
 aattctgttt tatcagaccg cttctgcgtt ctgatttaat ctgtatcagg ctgaaaatct 5131
 tctctcatcc gccaaaacag ccaagctac 5169
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<210> 39

<211> 757

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: pH3246

<400> 39

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 20 25 30

Gly Thr Gly Thr Gly Tyr Thr Met Asp Thr Val Asn Arg Thr His Gln
 35 40 45

Tyr Ser Glu Arg Gly Arg Trp Thr Thr Asn Thr Glu Thr Gly Ala Pro
 50 55 60

Gln Leu Asn Pro Ile Asp Gly Pro Leu Pro Glu Asp Asn Glu Pro Ser
 65 70 75 80

Gly Tyr Ala Gln Thr Asp Cys Val Leu Glu Ala Met Ala Phe Leu Glu
 85 90 95

Glu Ser His Pro Gly Ile Phe Glu Thr Ser Cys Leu Glu Thr Met Glu
 100 105 110

Val Val Gln Gln Thr Arg Val Asp Lys Leu Thr Gln Gly Arg Gln Thr
 115 120 125

Tyr Asp Trp Thr Leu Asn Arg Asn Gln Pro Ala Ala Thr Ala Leu Ala
 130 135 140
 Asn Thr Ile Glu Val Phe Arg Ser Asn Gly Leu Thr Ala Asn Glu Ser
 145 150 155 160
 Gly Arg Leu Ile Asp Phe Leu Lys Asp Val Met Glu Ser Met Asn Lys
 165 170 175
 Glu Glu Met Glu Ile Thr Thr His Phe Gln Arg Lys Arg Arg Val Arg
 180 185 190
 Asp Asn Met Thr Lys Lys Met Val Thr Gln Arg Thr Ile Gly Lys Arg
 195 200 205
 Lys Gln Arg Leu Asn Lys Arg Ser Tyr Leu Ile Arg Ala Leu Thr Leu
 210 215 220
 Asn Thr Met Thr Lys Asp Ala Glu Arg Gly Lys Leu Lys Arg Arg Ala
 225 230 235 240
 Ile Ala Thr Pro Gly Met Gln Ile Arg Gly Phe Val Tyr Phe Val Glu
 245 250 255
 Thr Leu Ala Arg Ser Ile Cys Glu Lys Leu Glu Gln Ser Gly Leu Pro
 260 265 270
 Val Gly Gly Asn Glu Lys Lys Ala Lys Leu Ala Asn Val Val Arg Lys
 275 280 285
 Met Met Thr Asn Ser Gln Asp Thr Glu Leu Ser Phe Thr Ile Thr Gly
 290 295 300
 Asp Asn Thr Lys Trp Asn Glu Asn Gln Asn Pro Arg Met Phe Leu Ala
 305 310 315 320
 Met Ile Thr Tyr Ile Thr Arg Asn Gln Pro Glu Trp Phe Arg Asn Val
 325 330 335
 Leu Ser Ile Ala Pro Ile Met Phe Ser Asn Lys Met Ala Arg Leu Gly
 340 345 350
 Lys Gly Tyr Met Phe Glu Ser Lys Ser Met Lys Leu Arg Thr Gln Ile
 355 360 365
 Pro Ala Glu Met Leu Ala Ser Ile Asp Leu Lys Tyr Phe Asn Asp Ser
 370 375 380
 Thr Arg Lys Lys Ile Glu Lys Ile Arg Pro Leu Leu Ile Asp Gly Thr
 385 390 395 400
 Ala Ser Leu Ser Pro Gly Met Met Met Gly Met Phe Asn Met Leu Ser
 405 410 415
 Thr Val Leu Gly Val Ser Ile Leu Asn Leu Gly Gln Lys Arg His Thr
 420 425 430
 Lys Thr Thr Tyr Trp Trp Asp Gly Leu Gln Ser Ser Asp Asp Phe Ala
 435 440 445
 Leu Ile Val Asn Ala Pro Asn His Glu Gly Ile Gln Ala Gly Val Asn
 450 455 460
 Arg Phe Tyr Arg Thr Cys Lys Leu Leu Gly Ile Asn Met Ser Lys Lys
 465 470 475 480

Lys Ser Tyr Ile Asn Arg Thr Gly Thr Phe Glu Phe Thr Ser Phe Phe
 485 490 495
 Tyr Arg Tyr Gly Phe Val Ala Asn Phe Ser Met Glu Leu Pro Ser Phe
 500 505 510
 Gly Val Ser Gly Ile Asn Glu Ser Ala Asp Met Ser Ile Gly Val Thr
 515 520 525
 Val Ile Lys Asn Asn Met Ile Asn Asn Asp Leu Gly Pro Ala Thr Ala
 530 535 540
 Gin Met Ala Leu Gln Leu Phe Ile Lys Asp Tyr Arg Tyr Thr Tyr Arg
 545 550 555 560
 Cys His Arg Gly Asp Thr Gln Ile Gln Thr Arg Arg Ser Phe Glu Ile
 565 570 575
 Lys Lys Leu Trp Glu Gln Thr His Ser Lys Ala Gly Leu Leu Val Ser
 580 585 590
 Asp Gly Gly Pro Asn Leu Tyr Asn Ile Arg Asn Leu His Ile Pro Glu
 595 600 605
 Val Cys Leu Lys Trp Glu Leu Met Asp Glu Asp Tyr Gln Gly Arg Leu
 610 615 620
 Cys Asn Pro Leu Asn Pro Phe Val Asn His Lys Asp Ile Glu Ser Val
 625 630 635 640
 Asn Asn Ala Val Ile Met Pro Ala His Gly Pro Ala Lys Asn Met Glu
 645 650 655
 Tyr Asp Ala Val Ala Thr Thr His Ser Trp Ile Pro Lys Arg Asn Arg
 660 665 670
 Ser Ile Leu Asn Thr Ser Gln Arg Gly Ile Leu Glu Asp Glu Gln Met
 675 680 685
 Tyr Gln Lys Cys Cys Asn Leu Phe Glu Lys Phe Phe Pro Ser Ser Ser
 690 695 700
 Tyr Arg Arg Pro Val Gly Ile Ser Ser Met Val Glu Ala Met Val Ser
 705 710 715 720
 Arg Ala Arg Ile Asp Ala Arg Ile Asp Phe Glu Ser Gly Arg Ile Lys
 725 730 735
 Lys Glu Glu Phe Thr Glu Ile Met Lys Ile Cys Ser Thr Ile Glu Glu
 740 745 750
 Leu Arg Arg Gln Lys
 755

<210> 40
 <211> 5169
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: pHL3247

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 <221> CDS
 <222> (191)..(2461)

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 acaaagggtc gcccggagta ctggtcgacc tccgaagttg ggggggagcg aaagcaggca 180
 aaccatgtga atg gat gtc aat ccg act tta ctt ttc tta aaa gtg cca 229
 Met Asp Val Asn Pro Thr Leu Leu Phe Leu Lys Val Pro
 1 5 10

gca caa aat gct ata agc aca act ttc cct tat act gga gac cct cct 277
 Ala Gln Asn Ala Ile Ser Thr Thr Phe Pro Tyr Thr Gly Asp Pro Pro
 15 20 25

tac agc cat ggg aca gga aca gga tac acc atg gat act gtc aac agg 325
 Tyr Ser His Gly Thr Gly Thr Gly Tyr Thr Met Asp Thr Val Asn Arg
 30 35 40 45

aca cat cag tac tca gaa agg gga aga tgg aca aca aac acc gaa act 373
 Thr His Gln Tyr Ser Glu Arg Gly Arg Trp Thr Thr Asn Thr Glu Thr
 50 55 60

gga gca ccg caa ctc aac ccg att gat ggg cca ctg cca gaa gac aat 421
 Gly Ala Pro Gln Leu Asn Pro Ile Asp Gly Pro Leu Pro Glu Asp Asn
 65 70 75

gaa cca agt ggt tat gcc caa aca gat tgt gta ttg gaa gca atg gcc 469
 Glu Pro Ser Gly Tyr Ala Gln Thr Asp Cys Val Leu Glu Ala Met Ala
 80 85 90

ttc ctt gag gaa tcc cat cct ggt atc ttt gag acc tcg tgt ctt gaa 517
 Phe Leu Glu Glu Ser His Pro Gly Ile Phe Glu Thr Ser Cys Leu Glu
 95 100 105

acg atg gag gtt gtt cag caa aca cga gtg gac aag ctg aca caa ggc 565
 Thr Met Glu Val Val Gln Gln Thr Arg Val Asp Lys Leu Thr Gln Gly
 110 115 120 125

cga cag acc tat gac tgg act cta aat agg aac cag cct gct gca aca 613
 Arg Gln Thr Tyr Asp Trp Thr Leu Asn Arg Asn Gln Pro Ala Ala Thr
 130 135 140

gca ttg gcc aac aca ata gaa gtg ttc aga tca aat ggc ctc acg gcc 661
 Ala Leu Ala Asn Thr Ile Glu Val Phe Arg Ser Asn Gly Leu Thr Ala
 145 150 155

aat gaa tct gga agg ctc ata gac ttc ctt aag gat gta atg gag tca 709
 Asn Glu Ser Gly Arg Leu Ile Asp Phe Leu Lys Asp Val Met Glu Ser
 160 165 170

atg aac aaa gaa gaa atg gag atc aca act cat ttt cag aga aag aga 757
 Met Asn Lys Glu Glu Met Glu Ile Thr Thr His Phe Gln Arg Lys Arg
 175 180 185

cga gtg aga gac aat atg act aag aaa atg gtg aca cag aga aca ata 805
 Arg Val Arg Asp Asn Met Thr Lys Lys Met Val Thr Gln Arg Thr Ile
 190 195 200 205

ggt aaa agg aag cag aga ttg aac aaa agg agt tat cta att agg gca 853
 Gly Lys Arg Lys Gln Arg Leu Asn Lys Arg Ser Tyr Leu Ile Arg Ala
 210 215 220

tta acc ctg aac aca atg acc aaa gat gct gag aga ggg aag cta aaa 901
 Leu Thr Leu Asn Thr Met Thr Lys Asp Ala Glu Arg Gly Lys Leu Lys
 225 230 235

cgg aga gca att gca acc cca ggg atg caa ata agg ggg ttt gta tac 949
 Arg Arg Ala Ile Ala Thr Pro Gly Met Gln Ile Arg Gly Phe Val Tyr
 240 245 250

ttt gtt gag aca cta gca agg agt ata tgt gag aaa ctt gaa caa tca 997
 Phe Val Glu Thr Leu Ala Arg Ser Ile Cys Glu Lys Leu Glu Gln Ser
 255 260 265

gga ttg cca gtt gga ggc aat gag aag aaa gca aag ttg gca aat gtt 1045
 Gly Leu Pro Val Gly Gly Asn Glu Lys Lys Aia Lys Leu Ala Asn Val
 270 275 280 285

gta agg aag atg atg acc aat tct cag gac act gaa att tct ttc acc 1093
 Val Arg Lys Met Met Thr Asn Ser Gln Asp Thr Glu Ile Ser Phe Thr
 290 295 300

atc act gga gat aac acc aaa tgg aac gaa aat cag aac cct cgg atg 1141
 Ile Thr Gly Asp Asn Thr Lys Trp Asn Glu Asn Gln Asn Pro Arg Met
 305 310 315

ttt ttg gcc atg atc aca tat ata acc aga aat cag ccc gaa tgg ttc 1189
 Phe Leu Ala Met Ile Thr Tyr Ile Thr Arg Asn Gln Pro Glu Trp Phe
 320 325 330

aga aat gtt cta agt att gct cca ata atg ttc tca aac aaa atg gcg 1237
 Arg Asn Val Leu Ser Ile Ala Pro Ile Met Phe Ser Asn Lys Met Ala
 335 340 345

aga ctg gga aag ggg tac atg ttt gag agc aag agt atg aaa att aga 1285
 Arg Leu Gly Lys Gly Tyr Met Phe Glu Ser Lys Ser Met Lys Ile Arg
 350 355 360 365

act caa ata cct gca gaa atg cta gca agt att gat cta aaa tat ttc 1333
 Thr Gln Ile Pro Ala Glu Met Leu Ala Ser Ile Asp Leu Lys Tyr Phe
 370 375 380

aat gaa cca aca agg aag aaa atc gag aaa ata agg cct ctc ata ata 1381
 Asn Glu Pro Thr Arg Lys Lys Ile Glu Lys Ile Arg Pro Leu Ile Ile
 385 390 395

gac ggc aca gcc tca tta agc ccg gga atg atg atg ggt atg ttc aac 1429
 Asp Gly Thr Ala Ser Leu Ser Pro Gly Met Met Met Gly Met Phe Asn
 400 405 410

atg ctg agt aca gtg ttg gga gtc tca atc ctg aat ctt ggg caa aag 1477
 Met Leu Ser Thr Val Leu Gly Val Ser Ile Leu Asn Leu Gly Gln Lys
 415 420 425

aga tac acc aaa acc aca tac tgg tgg gat gga ctt cag tcc tct gat 1525
 Arg Tyr Thr Lys Thr Tyr Trp Trp Asp Gly Leu Gln Ser Ser Asp
 430 435 440 445

gat ttt gct ctc atc gtg aat gca cca aat cat gag gga ata caa gcg 1573
 Asp Phe Ala Leu Ile Val Asn Ala Pro Asn His Glu Gly Ile Gln Ala
 450 455 460

gga gtg gat aga ttc tac aga acc tgc aag cta gtt ggg atc aat atg 1621
 Gly Val Asp Arg Phe Tyr Arg Thr Cys Lys Leu Val Gly Ile Asn Met
 465 470 475

agc aag aaa aag tcc tat ata aat agg aca gga aca ttc gaa ttc aca 1669
 Ser Lys Lys Ser Tyr Ile Asn Arg Thr Gly Thr Phe Glu Phe Thr
 480 485 490

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ccc agc ttt ggg gtg tct ggg atc aac gag tct gcg gac atg agt att Pro Ser Phe Gly Val Ser Gly Ile Asn Glu Ser Ala Asp Met Ser Ile 510 515 520 525	1765
gga gtt act gtc atc aaa aac aat atg ata aac aat gat ctt ggt cca Gly Val Thr Val Ile Lys Asn Asn Met Ile Asn Asn Asp Leu Gly Pro 530 535 540	1813
gca acc gct caa atg gcc ctt cag ctg ttc atc aaa gat tac agg tac Ala Thr Ala Gln Met Ala Leu Gln Leu Phe Ile Lys Asp Tyr Arg Tyr 545 550 555	1861
acg tac cgg tgc cat aga ggt gac aca caa ata caa acc cga aga tca Thr Tyr Arg Cys His Arg Gly Asp Thr Gln Ile Gln Thr Arg Arg Ser 560 565 570	1909
ttt gaa ata aag aaa ctg tgg gag caa acc cat tcc aaa gct gga ctg Phe Glu Ile Lys Lys Leu Trp Glu Gln Thr His Ser Lys Ala Gly Leu 575 580 585	1957
ctg gtc tcc gac gga ggc cca aat tta tac aac att aga aat ctc cac Leu Val Ser Asp Gly Gly Pro Asn Leu Tyr Asn Ile Arg Asn Leu His 590 595 600 605	2005
att cct gaa gtc tgc ttg aaa tgg gaa tta atg gat gag gat tac cag Ile Pro Glu Val Cys Leu Lys Trp Glu Leu Met Asp Glu Asp Tyr Gln 610 615 620	2053
ggg cgt tta tgc aac cca ctg aac cca ttt gtc aac cat aaa gac att Gly Arg Leu Cys Asn Pro Leu Asn Pro Phe Val Asn His Lys Asp Ile 625 630 635	2101
gaa tca gtg aac aat gca gtg ata atg cca gca cat ggt cca gcc aaa Glu Ser Val Asn Asn Ala Val Ile Met Pro Ala His Gly Pro Ala Lys 640 645 650	2149
aac atg gag tat gat gct gtt gca aca aca cac tcc tgg atc ccc aaa Asn Met Glu Tyr Asp Ala Val Ala Thr Thr His Ser Trp Ile Pro Lys 655 660 665	2197
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gaa caa atg tac caa aag tgc tgc aac tta ttt gaa aaa ttc ttc ccc Glu Gln Met Tyr Gln Lys Cys Cys Asn Leu Phe Glu Lys Phe Phe Pro 690 695 700	2293
agc agt tca tac aga aga cca gtc ggg ata tcc agt atg gtg gag gct Ser Ser Ser Tyr Arg Arg Pro Val Gly Ile Ser Ser Met Val Glu Ala 705 710 715	2341
atg gtt tcc aga gcc cga att gat gca cga att gat ttc gaa tct gga Met Val Ser Arg Ala Arg Ile Asp Ala Arg Ile Asp Phe Glu Ser Gly 720 725 730	2389
agg ata aag aaa gag gag ttc act gag atc atg aag atc tgt tcc acc Arg Ile Lys Lys Glu Glu Phe Thr Glu Ile Met Lys Ile Cys Ser Thr 735 740 745	2437
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 tcgccagatca atagttgcg caacgttggt gccattgcta caggcatcg ggtgtcacgc 4111
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 gtttacttc tgagttcggc atggggtagt gttggaccac cgcgtactg cggccaggca 5071
 aattctgttt tatcagaccg cttctgcgtt ctgatttaat ctgtatcagg ctgaaaatct 5131
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<210> 41

<211> 757

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: pH3247

<400> 41

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Gly Thr Gly Thr Gly Tyr Thr Met Asp Thr Val Asn Arg Thr His Gln
 35 40 45

Tyr Ser Glu Arg Gly Arg Trp Thr Thr Asn Thr Glu Thr Gly Ala Pro
 50 55 60

Gln Leu Asn Pro Ile Asp Gly Pro Leu Pro Glu Asp Asn Glu Pro Ser
 65 70 75 80

Gly Tyr Ala Gln Thr Asp Cys Val Leu Glu Ala Met Ala Phe Leu Glu
 85 90 95

Glu Ser His Pro Gly Ile Phe Glu Thr Ser Cys Leu Glu Thr Met Glu
 100 105 110

Val Val Gln Gln Thr Arg Val Asp Lys Leu Thr Gln Gly Arg Gln Thr
 115 120 125

Tyr Asp Trp Thr Leu Asn Arg Asn Gln Pro Ala Ala Thr Ala Leu Ala
 130 135 140

Asn Thr Ile Glu Val Phe Arg Ser Asn Gly Leu Thr Ala Asn Glu Ser
 145 150 155 160

Gly Arg Leu Ile Asp Phe Leu Lys Asp Val Met Glu Ser Met Asn Lys
 165 170 175

Glu Glu Met Glu Ile Thr Thr His Phe Gln Arg Lys Arg Arg Val Arg
 180 185 190

Asp Asn Met Thr Lys Lys Met Val Thr Gln Arg Thr Ile Gly Lys Arg
 195 200 205
 Lys Gln Arg Leu Asn Lys Arg Ser Tyr Leu Ile Arg Ala Leu Thr Leu
 210 215 220
 Asn Thr Met Thr Lys Asp Ala Glu Arg Gly Lys Leu Lys Arg Arg Ala
 225 230 235 240
 Ile Ala Thr Pro Gly Met Gln Ile Arg Gly Phe Val Tyr Phe Val Glu
 245 250 255
 Thr Leu Ala Arg Ser Ile Cys Glu Lys Leu Glu Gln Ser Gly Leu Pro
 260 265 270
 Val Gly Gly Asn Glu Lys Lys Ala Lys Leu Ala Asn Val Val Arg Lys
 275 280 285
 Met Met Thr Asn Ser Gln Asp Thr Glu Ile Ser Phe Thr Ile Thr Gly
 290 295 300
 Asp Asn Thr Lys Trp Asn Glu Asn Gln Asn Pro Arg Met Phe Leu Ala
 305 310 315 320
 Met Ile Thr Tyr Ile Thr Arg Asn Gln Pro Glu Trp Phe Arg Asn Val
 325 330 335
 Leu Ser Ile Ala Pro Ile Met Phe Ser Asn Lys Met Ala Arg Leu Gly
 340 345 350
 Lys Gly Tyr Met Phe Glu Ser Lys Ser Met Lys Ile Arg Thr Gln Ile
 355 360 365
 Pro Ala Glu Met Leu Ala Ser Ile Asp Leu Lys Tyr Phe Asn Glu Pro
 370 375 380
 Thr Arg Lys Lys Ile Glu Lys Ile Arg Pro Leu Ile Ile Asp Gly Thr
 385 390 395 400
 Ala Ser Leu Ser Pro Gly Met Met Gly Met Phe Asn Met Leu Ser
 405 410 415
 Thr Val Leu Gly Val Ser Ile Leu Asn Leu Gly Gln Lys Arg Tyr Thr
 420 425 430
 Lys Thr Thr Tyr Trp Trp Asp Gly Leu Gln Ser Ser Asp Asp Phe Ala
 435 440 445
 Leu Ile Val Asn Ala Pro Asn His Glu Gly Ile Gln Ala Gly Val Asp
 450 455 460
 Arg Phe Tyr Arg Thr Cys Lys Leu Val Gly Ile Asn Met Ser Lys Lys
 465 470 475 480
 Lys Ser Tyr Ile Asn Arg Thr Gly Thr Phe Glu Phe Thr Ser Phe Phe
 485 490 495
 Tyr Arg Tyr Gly Phe Val Ala Asn Phe Ser Met Glu Leu Pro Ser Phe
 500 505 510
 Gly Val Ser Gly Ile Asn Glu Ser Ala Asp Met Ser Ile Gly Val Thr
 515 520 525
 Val Ile Lys Asn Asn Met Ile Asn Asn Asp Leu Gly Pro Ala Thr Ala
 530 535 540

Gln Met Ala Leu Gln Leu Phe Ile Lys Asp Tyr Arg Tyr Thr Tyr Arg
 545 550 555 560
 Cys His Arg Gly Asp Thr Gln Ile Gln Thr Arg Arg Ser Phe Glu Ile
 565 570 575
 Lys Lys Leu Trp Glu Gln Thr His Ser Lys Ala Gly Leu Leu Val Ser
 580 585 590
 Asp Gly Gly Pro Asn Leu Tyr Asn Ile Arg Asn Leu His Ile Pro Glu
 595 600 605
 Val Cys Leu Lys Trp Glu Leu Met Asp Glu Asp Tyr Gln Gly Arg Leu
 610 615 620
 Cys Asn Pro Leu Asn Pro Phe Val Asn His Lys Asp Ile Glu Ser Val
 625 630 635 640
 Asn Asn Ala Val Ile Met Pro Ala His Gly Pro Ala Lys Asn Met Glu
 645 650 655
 Tyr Asp Ala Val Ala Thr Thr His Ser Trp Ile Pro Lys Arg Asn Arg
 660 665 670
 Ser Ile Leu Asn Thr Ser Gln Arg Gly Ile Leu Glu Asp Glu Gln Met
 675 680 685
 Tyr Gln Lys Cys Cys Asn Leu Phe Glu Lys Phe Phe Pro Ser Ser Ser
 690 695 700
 Tyr Arg Arg Pro Val Gly Ile Ser Ser Met Val Glu Ala Met Val Ser
 705 710 715 720
 Arg Ala Arg Ile Asp Ala Arg Ile Asp Phe Glu Ser Gly Arg Ile Lys
 725 730 735
 Lys Glu Glu Phe Thr Glu Ile Met Lys Ile Cys Ser Thr Ile Glu Glu
 740 745 750
 Leu Arg Arg Gln Lys
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<210> 42
 <211> 5169
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: pHL3258

<220>
 <221> CDS
 <222> (191)..(2461)

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 acaaagtgtc gcccggagta ctggtcgacc tccgaagttg ggggggagcg aaagcaggca 180
 aaccatttga atg gat gtc aat ccg act tta ctt ttc tta aaa gtg cca 229
 Met Asp Val Asn Pro Thr Leu Leu Phe Leu Lys Val Pro
 1 5 10

gca caa aat gct ata agc aca act ttc cct tat act gga gac cct cct		277
Ala Gln Asn Ala Ile Ser Thr Thr Phe Pro Tyr Thr Gly Asp Pro Pro		
15 20 25		
tac agc cat ggg aca gga aca gga tac acc atg gat act gtc aac agg		325
Tyr Ser His Gly Thr Gly Thr Gly Tyr Thr Met Asp Thr Val Asn Arg		
30 35 40 45		
aca cat cag tac tca gaa agg gga aga tgg aca aca aac acc gaa act		373
Thr His Gln Tyr Ser Glu Arg Gly Arg Trp Thr Thr Asn Thr Glu Thr		
50 55 60		
gga gca ccg caa ctc aac ccg att gat ggg cca ctg cca gaa gac aat		421
Gly Ala Pro Gln Leu Asn Pro Ile Asp Gly Pro Leu Pro Glu Asp Asn		
65 70 75		
gaa cca agt ggt tat gcc caa aca gat tgt gta ttg gaa gca atg gcc		469
Glu Pro Ser Gly Tyr Ala Gln Thr Asp Cys Val Leu Glu Ala Met Ala		
80 85 90		
ttc ctt gag gaa tcc cat cct ggt atc ttt gag acc tcg tgt ctt gaa		517
Phe Leu Glu Glu Ser His Pro Gly Ile Phe Glu Thr Ser Cys Leu Glu		
95 100 105		
acc atg gag gtt gtt cag caa aca cga gtg gac aag ctg aca caa ggc		565
Thr Met Glu Val Val Gln Gln Thr Arg Val Asp Lys Leu Thr Gln Gly		
110 115 120 125		
cga cag acc tat gac tgg act cta aat agg aac cag cct gct gca aca		613
Arg Gln Thr Tyr Asp Trp Thr Leu Asn Arg Asn Gln Pro Ala Ala Thr		
130 135 140		
gca ttg gcc aac aca ata gaa gtg ttc aga tca aat ggc ctc acg gcc		661
Ala Leu Ala Asn Thr Ile Glu Val Phe Arg Ser Asn Gly Leu Thr Ala		
145 150 155		
aat gaa tct gga agg ctc ata gac ttc ctt aag gat gta atg gag tca		709
Asn Glu Ser Gly Arg Leu Ile Asp Phe Leu Lys Asp Val Met Glu Ser		
160 165 170		
atg aac aaa gaa gaa atg gag atc aca act cat ttt cag aga aag aga		757
Met Asn Lys Glu Glu Met Glu Ile Thr Thr His Phe Gln Arg Lys Arg		
175 180 185		
cga gtg aga gac aat atg act aag aaa atg gtg aca cag aga aca ata		805
Arg Val Arg Asp Asn Met Thr Lys Lys Met Val Thr Gln Arg Thr Ile		
190 195 200 205		
ggt aaa agg aag cag aga ttg aac aaa agg agt tat cta att agg gca		853
Gly Lys Arg Lys Gln Arg Leu Asn Lys Arg Ser Tyr Leu Ile Arg Ala		
210 215 220		
ttt acc ctg aac aca atg acc aaa gat gct gag aga ggg aag cta aaa		901
Leu Thr Leu Asn Thr Met Thr Lys Asp Ala Glu Arg Gly Lys Leu Lys		
225 230 235		
ccg aga gca att gca acc cca ggg atg caa ata agg ggg ttt gta tac		949
Arg Arg Ala Ile Ala Thr Pro Gly Met Gln Ile Arg Gly Phe Val Tyr		
240 245 250		
ttt gtt gag aca cta gca agg agt ata tgt gag aaa ctt gaa caa tca		997
Phe Val Glu Thr Leu Ala Arg Ser Ile Cys Glu Lys Leu Glu Gln Ser		
255 260 265		
gga ttg cca gtt gga ggc aat gag aag aaa gca aag ttg gca aat gtt		1045
Gly Leu Pro Val Gly Gly Asn Glu Lys Ala Lys Leu Ala Asn Val		
270 275 280 285		

gta agg aag atg atg acc aat tct cag gac act gaa att tct ttc acc		1093	
Val Arg Lys Met Met Thr Asn Ser Gln Asp Thr Glu Ile Ser Phe Thr			
290	295	300	
atc act gga gat aac acc aaa tgg aac gaa aat cag aac cct cgg atg		1141	
Ile Thr Gly Asp Asn Thr Lys Trp Asn Glu Asn Gln Asn Pro Arg Met			
305	310	315	
ttt ttg gcc atg atc aca tat ata acc aga aat cag ccc gaa tgg ttc		1189	
Phe Leu Ala Met Ile Thr Tyr Ile Thr Arg Asn Gln Pro Glu Trp Phe			
320	325	330	
aga aat gtt cta agt att gct cca ata atg ttc tca aac aaa atg gcg		1237	
Arg Asn Val Leu Ser Ile Ala Pro Ile Met Phe Ser Asn Lys Met Ala			
335	340	345	
aga ctg gga aag ggg tac atg ttt gag agc aag agt atg aaa att aga		1285	
Arg Leu Gly Lys Gly Tyr Met Phe Glu Ser Lys Ser Met Lys Ile Arg			
350	355	360	365
act caa ata cct gca gaa atg cta gca agt att gat cta aaa tat ttc		1333	
Thr Gln Ile Pro Ala Glu Met Leu Ala Ser Ile Asp Leu Lys Tyr Phe			
370	375	380	
aat gaa cca aca agg aag aaa atc gag aaa ata agg cct ctc tta ata		1381	
Asn Glu Pro Thr Arg Lys Lys Ile Glu Lys Ile Arg Pro Leu Leu Ile			
385	390	395	
gat ggg act gca tca ttg agc cct gga atg atg atg ggc atg ttc aat		1429	
Asp Gly Thr Ala Ser Leu Ser Pro Gly Met Met Met Gly Met Phe Asn			
400	405	410	
atg tta agt act gta tta ggc gtc tcc atc ctg aat ctt gga caa aag		1477	
Met Leu Ser Thr Val Leu Gly Val Ser Ile Leu Asn Leu Gly Gln Lys			
415	420	425	
aga cac acc aag act act tac tgg tgg gat ggt ctt caa tct tct gat		1525	
Arg His Thr Lys Thr Tyr Trp Trp Asp Gly Leu Gln Ser Ser Asp			
430	435	440	445
gat ttt gct ctg att gtg aat gca ccc aat cat gaa ggg att caa gcc		1573	
Asp Phe Ala Leu Ile Val Asn Ala Pro Asn His Glu Gly Ile Gln Ala			
450	455	460	
gga gtc aac agg ttt tat cga acc tgt aag cta ctt gga att aat atg		1621	
Gly Val Asn Arg Phe Tyr Arg Thr Cys Lys Leu Leu Gly Ile Asn Met			
465	470	475	
agc aag aaa aag tct tac ata aac aga aca ggt aca ttt gaa ttc aca		1669	
Ser Lys Lys Ser Tyr Ile Asn Arg Thr Gly Thr Phe Glu Phe Thr			
480	485	490	
agc ttt ttc tat cgt tat ggg ttt gtt gcc aat ttc agc atg gag ctt		1717	
Ser Phe Phe Tyr Arg Tyr Gly Phe Val Ala Asn Phe Ser Met Glu Leu			
495	500	505	
ccc agc ttt ggg gtg tct ggg atc aac gag tct gcg gac atg agt att		1765	
Pro Ser Phe Gly Val Ser Gly Ile Asn Glu Ser Ala Asp Met Ser Ile			
510	515	520	525
gga gtt act gtc atc aaa aac aat atg ata aac aat gat ctt ggt cca		1813	
Gly Val Thr Val Ile Lys Asn Asn Met Ile Asn Asn Asp Leu Gly Pro			
530	535	540	
gca acc gct caa atg gcc ctt cag ctg ttc atc aaa gat tac agg tac		1861	

Ala Thr Ala Gln Met Ala Leu Gln Leu Phe Ile Lys Asp Tyr Arg Tyr
 545 550 555

acg tac cgg tgc cat aga ggt gac aca caa ata caa acc cga aga tca 1909
 Thr Tyr Arg Cys His Arg Gly Asp Thr Gln Ile Gln Thr Arg Arg Ser
 560 565 570

ttt gaa ata aag aaa ctg tgg gag caa acc cat tcc aaa gct gga ctg 1957
 Phe Glu Ile Lys Lys Leu Trp Glu Gln Thr His Ser Lys Ala Gly Leu
 575 580 585

ctg gtc tcc gac gga ggc cca aat tta tac aac att aga aat ctc cac 2005
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 590 595 600 605

att cct gaa gtc tgc ttg aaa tgg gaa tta atg gat gag gat tac cag 2053
 Ile Pro Glu Val Cys Leu Lys Trp Glu Leu Met Asp Glu Asp Tyr Gln
 610 615 620

ggg cgt tta tgc aac cca ctg aac cca ttt gtc aac cat aaa gac att 2101
 Gly Arg Leu Cys Asn Pro Leu Asn Pro Phe Val Asn His Lys Asp Ile
 625 630 635

gaa tca gtg aac aat gca gtg ata atg cca gca cat ggt cca gcc aza 2149
 Glu Ser Val Asn Asn Ala Val Ile Met Pro Ala His Gly Pro Ala Lys
 640 645 650

aac atg gag tat gat gct gtt gca aca aca cac tcc tgg atc ccc aza 2197
 Asn Met Glu Tyr Asp Ala Val Ala Thr Thr His Ser Trp Ile Pro Lys
 655 660 665

aga aat cga tcc atc ttg aat aca agc caa aga gga ata ctt gaa gat 2245
 Arg Asn Arg Ser Ile Leu Asn Thr Ser Gln Arg Gly Ile Leu Glu Asp
 670 675 680 685

gaa caa atg tac caa aag tgc tgc aac tta ttt gaa aaa ttc ttc ccc 2293
 Glu Gln Met Tyr Gln Lys Cys Cys Asn Leu Phe Glu Lys Phe Phe Pro
 690 695 700

agc agt tca tac aga aga cca gtc ggg ata tcc agt atg gtg gag gct 2341
 Ser Ser Ser Tyr Arg Arg Pro Val Gly Ile Ser Ser Met Val Glu Ala
 705 710 715

atg gtt tcc aga gcc cga att gat gca cga att gat ttc gaa tct gga 2389
 Met Val Ser Arg Ala Arg Ile Asp Ala Arg Ile Asp Phe Glu Ser Gly
 720 725 730

agg ata aag aaa gag gag ttc act gag atc atg aag atc tgt tcc acc 2437
 Arg Ile Lys Lys Glu Glu Phe Thr Glu Ile Met Lys Ile Cys Ser Thr
 735 740 745

att gaa gag ctc aga cgg caa aaa tagtgaattt agcttgcct tcataaaaaa 2491
 Ile Glu Glu Leu Arg Arg Gln Lys
 750 755

atgccttgtt tctactaata acccgccggc ccaaatgcc gactcggagc gaaagatata 2551

cctcccccgg ggccgggagg tcgcgtcacc gaccacgccc cggcccgagg cgacgcgcga 2611

cacggacacc tgtccccaaa aacgcccacca tcgcagccac acacggagcg cccggggccc 2671

tctggtaac cccaggacac acgcgggagc agcgccggc cggggacgccc cttccggccg 2731

cccgtgccac acgcaggggg ccggcccggtg tctccagagc gggagccgga agcattttcg 2791

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 tagaaaaata aacaaaagag ttgttagaaa cgcaaaaagg ccatccgtca ggtggcctt 4771
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 ttgttcgca acgttcaaatt ccgttccgg cggatttgc ctactcagga gagcgttac 4891

cgacaaaacaa cagataaaaac gaaaggccca gtcttcgac tgagctttc gtttatgg 4951
 atgcctggca gttccctact ctcgcattgg gagaacccac actaccatcg gcgctacggc 5011
 gtttcacttc tgagttcggc atggggtcag gtgggaccac cgcgctactg ccggcaggca 5071
 aattctgttt tatcagaccg cttctgcgtt ctgatttaat ctgtatcagg ctgaaaatct 5131
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<210> 43

<211> 757

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: pH3258

<400> 43

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 20 25 30

Gly Thr Gly Thr Gly Tyr Thr Met Asp Thr Val Asn Arg Thr His Gln
 35 40 45

Tyr Ser Glu Arg Gly Arg Trp Thr Thr Asn Thr Glu Thr Gly Ala Pro
 50 55 60

Gln Leu Asn Pro Ile Asp Gly Pro Leu Pro Glu Asn Glu Pro Ser
 65 70 75 80

Gly Tyr Ala Gln Thr Asp Cys Val Leu Glu Ala Met Ala Phe Leu Glu
 85 90 95

Glu Ser His Pro Gly Ile Phe Glu Thr Ser Cys Leu Glu Thr Met Glu
 100 105 110

Val Val Gln Gln Thr Arg Val Asp Lys Leu Thr Gln Gly Arg Gln Thr
 115 120 125

Tyr Asp Trp Thr Leu Asn Arg Asn Gln Pro Ala Ala Thr Ala Leu Ala
 130 135 140

Asn Thr Ile Glu Val Phe Arg Ser Asn Gly Leu Thr Ala Asn Glu Ser
 145 150 155 160

Gly Arg Leu Ile Asp Phe Leu Lys Asp Val Met Glu Ser Met Asn Lys
 165 170 175

Glu Glu Met Glu Ile Thr Thr His Phe Gln Arg Lys Arg Arg Val Arg
 180 185 190

Asp Asn Met Thr Lys Lys Met Val Thr Gln Arg Thr Ile Gly Lys Arg
 195 200 205

Lys Gln Arg Leu Asn Lys Arg Ser Tyr Leu Ile Arg Ala Leu Thr Leu
 210 215 220

Asn Thr Met Thr Lys Asp Ala Glu Arg Gly Lys Leu Lys Arg Arg Ala
 225 230 235 240

Ile Ala Thr Pro Gly Met Gln Ile Arg Gly Phe Val Tyr Phe Val Glu
 245 250 255

Thr Leu Ala Arg Ser Ile Cys Glu Lys Leu Glu Gln Ser Gly Leu Pro
 260 265 270
 Val Gly Gly Asn Glu Lys Lys Ala Lys Leu Ala Asn Val Val Arg Lys
 275 280 285
 Met Met Thr Asn Ser Gln Asp Thr Glu Ile Ser Phe Thr Ile Thr Gly
 290 295 300
 Asp Asn Thr Lys Trp Asn Glu Asn Gln Asn Pro Arg Met Phe Leu Ala
 305 310 315 320
 Met Ile Thr Tyr Ile Thr Arg Asn Gln Pro Glu Trp Phe Arg Asn Val
 325 330 335
 Leu Ser Ile Ala Pro Ile Met Phe Ser Asn Lys Met Ala Arg Leu Gly
 340 345 350
 Lys Gly Tyr Met Phe Glu Ser Lys Ser Met Lys Ile Arg Thr Gln Ile
 355 360 365
 Pro Ala Glu Met Leu Ala Ser Ile Asp Leu Lys Tyr Phe Asn Glu Pro
 370 375 380
 Thr Arg Lys Lys Ile Glu Lys Ile Arg Pro Leu Leu Ile Asp Gly Thr
 385 390 395 400
 Ala Ser Leu Ser Pro Gly Met Met Gly Met Phe Asn Met Leu Ser
 405 410 415
 Thr Val Leu Gly Val Ser Ile Leu Asn Leu Gly Gln Lys Arg His Thr
 420 425 430
 Lys Thr Thr Tyr Trp Trp Asp Gly Leu Gln Ser Ser Asp Asp Phe Ala
 435 440 445
 Leu Ile Val Asn Ala Pro Asn His Glu Gly Ile Gln Ala Gly Val Asn
 450 455 460
 Arg Phe Tyr Arg Thr Cys Lys Leu Leu Gly Ile Asn Met Ser Lys Lys
 465 470 475 480
 Lys Ser Tyr Ile Asn Arg Thr Gly Thr Phe Glu Phe Thr Ser Phe Phe
 485 490 495
 Tyr Arg Tyr Gly Phe Val Ala Asn Phe Ser Met Glu Leu Pro Ser Phe
 500 505 510
 Gly Val Ser Gly Ile Asn Glu Ser Ala Asp Met Ser Ile Gly Val Thr
 515 520 525
 Val Ile Lys Asn Asn Met Ile Asn Asn Asp Leu Gly Pro Ala Thr Ala
 530 535 540
 Gln Met Ala Leu Gln Leu Phe Ile Lys Asp Tyr Arg Tyr Thr Tyr Arg
 545 550 555 560
 Cys His Arg Gly Asp Thr Gln Ile Gln Thr Arg Arg Ser Phe Glu Ile
 565 570 575
 Lys Lys Leu Trp Glu Gln Thr His Ser Lys Ala Gly Leu Leu Val Ser
 580 585 590
 Asp Gly Gly Pro Asn Leu Tyr Asn Ile Arg Asn Leu His Ile Pro Glu
 595 600 605

Val Cys Leu Lys Trp Glu Leu Met Asp Glu Asp Tyr Gln Gly Arg Leu
 610 615 620

Cys Asn Pro Leu Asn Pro Phe Val Asn His Lys Asp Ile Glu Ser Val
 625 630 635 640

Asn Asn Ala Val Ile Met Pro Ala His Gly Pro Ala Lys Asn Met Glu
 645 650 655

Tyr Asp Ala Val Ala Thr Thr His Ser Trp Ile Pro Lys Arg Asn Arg
 660 665 670

Ser Ile Leu Asn Thr Ser Gln Arg Gly Ile Leu Glu Asp Glu Gln Met
 675 680 695

Tyr Gln Lys Cys Cys Asn Leu Phe Glu Lys Phe Phe Pro Ser Ser Ser
 690 695 700

Tyr Arg Arg Pro Val Gly Ile Ser Ser Met Val Glu Ala Met Val Ser
 705 710 715 720

Arg Ala Arg Ile Asp Ala Arg Ile Asp Phe Glu Ser Gly Arg Ile Lys
 725 730 735

Lys Glu Glu Phe Thr Glu Ile Met Lys Ile Cys Ser Thr Ile Glu Glu
 740 745 750

Leu Arg Arg Gln Lys
 755

<210> 44

<211> 5169

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: pH3259

<220>

<221> CDS

<222> (191)..(2461)

<400> 44

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acaaaagtgtc gcccggagta ctggtcgacc tccgaagttt ggggggagcgc aaagcaggca 180

aaccatttga atg gat gtc aat ccg act tta ctt ttc tta aaa gtg cca 229
 Met Asp Val Asn Pro Thr Leu Leu Phe Leu Lys Val Pro

1

5

10

gca caa aat gct ata agc aca act ttc cct tat act gga gac cct cct 277
 Ala Gln Asn Ala Ile Ser Thr Thr Phe Pro Tyr Thr Gly Asp Pro Pro

15

20

25

tac agc cat ggg aca gga aca gga tac acc atg gat act gtc aac agg 325
 Tyr Ser His Gly Thr Gly Thr Gly Tyr Thr Met Asp Thr Val Asn Arg

30

35

40

45

aca cat cag tac tca gaa agg gga aga tgg acà aca aac acc gaa act 373
 Thr His Gln Tyr Ser Glu Arg Gly Arg Trp Thr Thr Asn Thr Glu Thr

50

55

60

gga gca ccg caa ctc aac ccg att gat ggg cca ctg cca gaa gac aat Gly Ala Pro Gln Leu Asn Pro Ile Asp Gly Pro Leu Pro Glu Asp Asn 65 70 75	421
gaa cca act ggt tat gcc caa aca gat tgt gta ttg gaa gca atg gcc Glu Pro Ser Gly Tyr Ala Gln Thr Asp Cys Val Leu Glu Ala Met Ala 80 85 90	469
ttc ctt gag gaa tcc cat cct ggt atc ttt gag acc tcg tgt ctt gaa Phe Leu Glu Glu Ser His Pro Gly Ile Phe Glu Thr Ser Cys Leu Glu 95 100 105	517
acg atg gag gtt gtt cag caa aca cga gtg gac aag ctg aca caa ggc Thr Met Glu Val Val Gln Gln Thr Arg Val Asp Lys Leu Thr Gln Gly 110 115 120 125	565
cga cag acc tat gac tgg act cta aat agg aac cag cct gct gca aca Arg Gln Thr Tyr Asp Trp Thr Leu Asn Arg Asn Gln Pro Ala Ala Thr 130 135 140	613
gca ttg gcc aac aca ata gaa gtg ttc aga tca aat ggc ctc acg gcc Ala Leu Ala Asn Thr Ile Glu Val Phe Arg Ser Asn Gly Leu Thr Ala 145 150 155	661
aat gaa tct gga agg ctc ata gac ttc ctt aag gat gta atg gag tca Asn Glu Ser Gly Arg Leu Ile Asp Phe Leu Lys Asp Val Met Glu Ser 160 165 170	709
atg aac aaa gaa gaa atg gag atc aca act cat ttt cag aga aag aga Met Asn Lys Glu Glu Met Glu Ile Thr Thr His Phe Gln Arg Lys Arg 175 180 185	757
cga gtg aga gac aat atg act aag aaa atg gtg aca cag aga aca ata Arg Val Arg Asp Asn Met Thr Lys Lys Met Val Thr Gln Arg Thr Ile 190 195 200 205	805
ggt aaa aca aag cag aga ttg aac aaa agg agt tat cta att agg gca Gly Lys Arg Lys Gln Arg Leu Asn Lys Arg Ser Tyr Leu Ile Arg Ala 210 215 220	853
tta acc ctg aac aca atg acc aaa gat gct gag aga ggg aag cta aaa Leu Thr Leu Asn Thr Met Thr Lys Asp Ala Glu Arg Gly Lys Leu Lys 225 230 235	901
cgg aga gca att gca acc cca ggg atg caa ata agg ggg ttt gta tac Arg Arg Ala Ile Ala Thr Pro Gly Met Gln Ile Arg Gly Phe Val Tyr 240 245 250	949
ttt gtt gag aca cta gca agg agt ata tgt gag aaa ctt gaa caa tca Phe Val Glu Thr Leu Ala Arg Ser Ile Cys Glu Lys Leu Glu Gln Ser 255 260 265	997
gga ttg cca gtt gga ggc aat gag aag aaa gca aag ttg gca aat gtt Gly Leu Pro Val Gly Gly Asn Glu Lys Lys Ala Lys Leu Ala Asn Val 270 275 280 285	1045
gta agg aac atg atg acc aat tct cag gac act gaa att tct ttc acc Val Arg Lys Met Met Thr Asn Ser Gln Asp Thr Glu Ile Ser Phe Thr 290 295 300	1093
atc act gca gat aac acc aaa tgg aac gaa aat cag aac cct cgg atg Ile Thr Gly Asp Asn Thr Lys Trp Asn Glu Asn Gln Asn Pro Arg Met 305 310 315	1141
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aga aat gtt cta agt att gct cca ata atg ttc tca aac aaa atg gcg	1237
Arg Asn Val Leu Ser Ile Ala Pro Ile Met Phe Ser Asn Lys Met Ala	
335 340 345	
aga ctg gga aag ggg tac atg ttt gag agc aag agt atg aaa att aga	1285
Arg Leu Gly Lys Gly Tyr Met Phe Glu Ser Lys Ser Met Lys Ile Arg	
350 355 360 365	
act caa ata cct gca gaa atg cta gca agt att gat cta aaa tat ttc	1333
Thr Gln Ile Pro Ala Glu Met Leu Ala Ser Ile Asp Leu Lys Tyr Phe	
370 375 380	
aat gaa cca aca agg aag aaa atc gag aaa ata agg cct ctc tta ata	1381
Asn Glu Pro Thr Arg Lys Lys Ile Glu Lys Ile Arg Pro Leu Leu Ile	
385 390 395	
gat ggg act gca tca ttg agc cct gga atg atg atg ggc atg ttc aat	1429
Asp Gly Thr Ala Ser Leu Ser Pro Gly Met Met Gly Met Phe Asn	
400 405 410	
atg tta agt act gta tta ggc gtc tcc atc ctg aat ctt gga caa aag	1477
Met Leu Ser Thr Val Leu Gly Val Ser Ile Leu Asn Leu Gly Gln Lys	
415 420 425	
aga cac acc aag act act tac tgg tgg gat ggt ctt caa tct tct gat	1525
Arg His Thr Lys Thr Tyr Trp Trp Asp Gly Leu Gln Ser Ser Asp	
430 435 440 445	
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Asp Phe Ala Leu Ile Val Asn Ala Pro Asn His Glu Gly Ile Gln Ala	
450 455 460	
gga gtc aac agg ttt tat cga acc tgt aag cta ctt gga att aat atg	1621
Gly Val Asn Arg Phe Tyr Arg Thr Cys Lys Leu Leu Gly Ile Asn Met	
465 470 475	
agc aag aaa aag tct tac ata aac aga aca ggt aca ttt gaa ttc aca	1669
Ser Lys Lys Ser Tyr Ile Asn Arg Thr Gly Thr Phe Glu Phe Thr	
480 485 490	
agc ttt ttc tac cgc tat gga ttt gta gcc aat ttt agt atg gag ttg	1717
Ser Phe Phe Tyr Arg Tyr Gly Phe Val Ala Asn Phe Ser Met Glu Leu	
495 500 505	
ccc agc ttt gga gta tca gga att aat gaa tcg gct gat atg agc att	1765
Pro Ser Phe Gly Val Ser Gly Ile Asn Glu Ser Ala Asp Met Ser Ile	
510 515 520 525	
gga gta aca gtg ata aag aat aac atg ata aac aat gat ctt gga ccg	1813
Gly Val Thr Val Ile Lys Asn Asn Met Ile Asn Asn Asp Leu Gly Pro	
530 535 540	
gca aca gcc caa atg gct ctc caa tta ttc atc aag gac tac aga tat	1861
Ala Thr Ala Gln Met Ala Leu Gln Leu Phe Ile Lys Asp Tyr Arg Tyr	
545 550 555	
aca tac agg tgt cac agg gga gac aca caa atc caa acg agg agg tca	1909
Thr Tyr Arg Cys His Arg Gly Asp Thr Gln Ile Gln Thr Arg Arg Ser	
560 565 570	
ttc gag cta aag aag ctg tgg gag cag acc cgc tca aag gca gga ctg	1957
Phe Glu Leu Lys Lys Leu Trp Glu Gln Thr Arg Ser Lys Ala Gly Leu	
575 580 585	

ttg gtt tca gat ggc gga cca aac ctg tac aac att cga aat ctc cac	590	595	600	605	2005
Leu Val Ser Asp Gly Gly Pro Asn Leu Tyr Asn Ile Arg Asn Leu His					
att cct gaa gtc tgc ttg aaa tgg gaa tta atg gat gag gat tac cag	610	615	620		2053
Ile Pro Glu Val Cys Leu Lys Trp Glu Leu Met Asp Glu Asp Tyr Gln					
ggg cgt tta tgc aac cca ctg aac cca ttt gtc aac cat aaa gac att	625	630	635		2101
Gly Arg Leu Cys Asn Pro Leu Asn Pro Phe Val Asn His Lys Asp Ile					
gaa tca gtg aac aat gca gtg ata atg cca gca cat ggt cca gcc aaa	640	645	650		2149
Glu Ser Val Asn Asn Ala Val Ile Met Pro Ala His Gly Pro Ala Lys					
aac atg gag tat gat gct gtt gca aca aca cac tcc tgg atc ccc aaa	655	660	665		2197
Asn Met Glu Tyr Asp Ala Val Ala Thr Thr His Ser Trp Ile Pro Lys					
aga aat cga tcc atc ttg aat aca agc caa aga gga ata ctt gaa gat	670	675	680	685	2245
Arg Asn Arg Ser Ile Leu Asn Thr Ser Gln Arg Gly Ile Leu Glu Asp					
gaa caa atg tac caa aag tgc tgc aac tta ttt gaa aaa ttc ttc ccc	690	695	700		2293
Glu Gln Met Tyr Gln Lys Cys Cys Asn Leu Phe Glu Lys Phe Phe Pro					
agc agt tca tac aga aga cca gtc ggg ata tcc agt atg gtg gag gct	705	710	715		2341
Ser Ser Ser Tyr Arg Arg Pro Val Gly Ile Ser Ser Met Val Glu Ala					
atg gtt tcc aga gcc cga att gat gca cga att gat ttc gaa tct gga	720	725	730		2389
Met Val Ser Arg Ala Arg Ile Asp Ala Arg Ile Asp Phe Glu Ser Gly					
agg ata aag aaa gag gag ttc act gag atc atg aag atc tgt tcc acc	735	740	745		2437
Arg Ile Lys Lys Glu Glu Phe Thr Glu Ile Met Lys Ile Cys Ser Thr					
att gaa gag ctc aga cgg caa aaa tagtgaattt agcttgcct tcataaaaaaa	750	755			2491
Ile Glu Glu Leu Arg Arg Gln Lys					
atgccttgtt tctactaata acccgccggc ccaaatgcc gactcgagc gaaagatata					2551
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<211> 757

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: pH3259

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20 25 30Gly Thr Gly Thr Gly Tyr Thr Met Asp Thr Val Asn Arg Thr His Gln
35 40 45Tyr Ser Glu Arg Gly Arg Trp Thr Thr Asn Thr Glu Thr Gly Ala Pro
50 55 60Gln Leu Asn Pro Ile Asp Gly Pro Leu Pro Glu Asp Asn Glu Pro Ser
65 70 75 80Gly Tyr Ala Gln Thr Asp Cys Val Leu Glu Ala Met Ala Phe Leu Glu
85 90 95Glu Ser His Pro Gly Ile Phe Glu Thr Ser Cys Leu Glu Thr Met Glu
100 105 110Val Val Gln Gln Thr Arg Val Asp Lys Leu Thr Gln Gly Arg Gln Thr
115 120 125Tyr Asp Trp Thr Leu Asn Arg Asn Gln Pro Ala Ala Thr Ala Leu Ala
130 135 140Asn Thr Ile Glu Val Phe Arg Ser Asn Gly Leu Thr Ala Asn Glu Ser
145 150 155 160Gly Arg Leu Ile Asp Phe Leu Lys Asp Val Met Glu Ser Met Asn Lys
165 170 175Glu Glu Met Glu Ile Thr Thr His Phe Gln Arg Lys Arg Arg Val Arg
180 185 190Asp Asn Met Thr Lys Lys Met Val Thr Gln Arg Thr Ile Gly Lys Arg
195 200 205Lys Gln Arg Leu Asn Lys Arg Ser Tyr Leu Ile Arg Ala Leu Thr Leu
210 215 220Asn Thr Met Thr Lys Asp Ala Glu Arg Gly Lys Leu Lys Arg Arg Ala
225 230 235 240Ile Ala Thr Pro Gly Met Gln Ile Arg Gly Phe Val Tyr Phe Val Glu
245 250 255Thr Leu Ala Arg Ser Ile Cys Glu Lys Leu Glu Gln Ser Gly Leu Pro
260 265 270Val Gly Gly Asn Glu Lys Lys Ala Lys Leu Ala Asn Val Val Arg Lys
275 280 285Met Met Thr Asn Ser Gln Asp Thr Glu Ile Ser Phe Thr Ile Thr Gly
290 295 300Asp Asn Thr Lys Trp Asn Glu Asn Gln Asn Pro Arg Met Phe Leu Ala
305 310 315 320

Met Ile Thr Tyr Ile Thr Arg Asn Gln Pro Glu Trp Phe Arg Asn Val
 325 330 335
 Leu Ser Ile Ala Pro Ile Met Phe Ser Asn Lys Met Ala Arg Leu Gly
 340 345 350
 Lys Gly Tyr Met Phe Glu Ser Lys Ser Met Lys Ile Arg Thr Gln Ile
 355 360 365
 Pro Ala Glu Met Leu Ala Ser Ile Asp Leu Lys Tyr Phe Asn Glu Pro
 370 375 380
 Thr Arg Lys Lys Ile Glu Lys Ile Arg Pro Leu Leu Ile Asp Gly Thr
 385 390 395 400
 Ala Ser Leu Ser Pro Gly Met Met Gly Met Phe Asn Met Leu Ser
 405 410 415
 Thr Val Leu Gly Val Ser Ile Leu Asn Leu Gly Gln Lys Arg His Thr
 420 425 430
 Lys Thr Thr Tyr Trp Trp Asp Gly Leu Gln Ser Ser Asp Asp Phe Ala
 435 440 445
 Leu Ile Val Asn Ala Pro Asn His Glu Gly Ile Gln Ala Gly Val Asn
 450 455 460
 Arg Phe Tyr Arg Thr Cys Lys Leu Leu Gly Ile Asn Met Ser Lys Lys
 465 470 475 480
 Lys Ser Tyr Ile Asn Arg Thr Gly Thr Phe Glu Phe Thr Ser Phe Phe
 485 490 495
 Tyr Arg Tyr Gly Phe Val Ala Asn Phe Ser Met Glu Leu Pro Ser Phe
 500 505 510
 Gly Val Ser Gly Ile Asn Glu Ser Ala Asp Met Ser Ile Gly Val Thr
 515 520 525
 Val Ile Lys Asn Asn Met Ile Asn Asn Asp Leu Gly Pro Ala Thr Ala
 530 535 540
 Gln Met Ala Leu Gln Leu Phe Ile Lys Asp Tyr Arg Tyr Thr Tyr Arg
 545 550 555 560
 Cys His Arg Gly Asp Thr Gln Ile Gln Thr Arg Arg Ser Phe Glu Leu
 565 570 575
 Lys Lys Leu Trp Glu Gln Thr Arg Ser Lys Ala Gly Leu Leu Val Ser
 580 585 590
 Asp Gly Gly Pro Asn Leu Tyr Asn Ile Arg Asn Leu His Ile Pro Glu
 595 600 605
 Val Cys Leu Lys Trp Glu Leu Met Asp Glu Asp Tyr Gln Gly Arg Leu
 610 615 620
 Cys Asn Pro Leu Asn Pro Phe Val Asn His Lys Asp Ile Glu Ser Val
 625 630 635 640
 Asn Asn Ala Val Ile Met Pro Ala His Gly Pro Ala Lys Asn Met Glu
 645 650 655
 Tyr Asp Ala Val Ala Thr Thr His Ser Trp Ile Pro Lys Arg Asn Arg
 660 665 670

Ser Ile Leu Asn Thr Ser Gln Arg Gly Ile Leu Glu Asp Glu Gln Met
 675 680 685

Tyr Gln Lys Cys Cys Asn Leu Phe Glu Lys Phe Phe Pro Ser Ser Ser
 690 695 700

Tyr Arg Arg Pro Val Gly Ile Ser Ser Met Val Glu Ala Met Val Ser
 705 710 715 720

Arg Ala Arg Ile Asp Ala Arg Ile Asp Phe Glu Ser Gly Arg Ile Lys
 725 730 735

Lys Glu Glu Phe Thr Glu Ile Met Lys Ile Cys Ser Thr Ile Glu Glu
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Leu Arg Arg Gln Lys
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<211> 5169

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: pH3268

<220>

<221> CDS

<222> (191)...(2461)

<400> 46

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acaaagtgtc gcccggagta ctggtcgacc tccgaagttg ggggggagcg aaagcaggca 180

aaccatttga atg gat gtc aat ccg act tta ctt ttc tta aaa gtg cca 229
 Met Asp Val Asn Pro Thr Leu Leu Phe Leu Lys Val Pro
 1 5 10

gca caa aat gct ata agc aca act ttc cct tat act gga gac cct cct 277
 Ala Gln Asn Ala Ile Ser Thr Thr Phe Pro Tyr Thr Gly Asp Pro Pro
 15 20 25

tac agc cat ggg aca gga aca gga tac acc atg gat act gtc aac agg 325
 Tyr Ser His Gly Thr Gly Thr Tyr Thr Met Asp Thr Val Asn Arg
 30 35 40 45

aca cat cag tac tca gaa agg gga aga tgg aca aca aac acc gaa act 373
 Thr His Gln Tyr Ser Glu Arg Gly Arg Trp Thr Thr Asn Thr Glu Thr
 50 55 60

gga gca ccg caa ctc aac ccg att gat ggg cca ctg cca gaa gac aat 421
 Gly Ala Pro Gln Leu Asn Pro Ile Asp Gly Pro Leu Pro Glu Asp Asn
 65 70 75

gaa cca agt ggt tat gcc caa aca gat tgt gta ttg gaa gca atg gcc 469
 Glu Pro Ser Gly Tyr Ala Gln Thr Asp Cys Val Leu Glu Ala Met Ala
 80 85 90

ttc ctt gag gaa tcc cat cct ggt atc ttt gag acc tcg tgt ctt gaa 517
 Phe Leu Glu Glu Ser His Pro Gly Ile Phe Glu Thr Ser Cys Leu Glu
 95 100 105

acg atg gag gtt cag caa aca cga gtg gac aag ctg aca caa ggc 565

Thr Met Glu Val Val Gln Gln Thr Arg Val Asp Lys Leu Thr Gln Gly																																																																																																																																																														
110	115	120	125			cg a cag acc tat gac tgg act cta aat agg aac cag cct gct gca aca		613	Arg Gln Thr Tyr Asp Trp Thr Leu Asn Arg Asn Gln Pro Ala Ala Thr			130	135	140	gca ttg gcc aac aca ata gaa gtg ttc aga tca aat ggc ctc acg gcc		661	Ala Leu Ala Asn Thr Ile Glu Val Phe Arg Ser Asn Gly Leu Thr Ala			145	150	155	aat gaa tct gga agg ctc ata gac ttc ctt aag gat gta atg gag tca		709	Asn Glu Ser Gly Arg Leu Ile Asp Phe Leu Lys Asp Val Met Glu Ser			160	165	170	atg aac aaa gaa gaa atg gag atc aca act cat ttt cag aga aag aga		757	Met Asn Lys Glu Glu Met Glu Ile Thr Thr His Phe Gln Arg Lys Arg			175	180	185	cga gtg aga gac aat atg act aag aaa atg gtg aca cag aga aca ata		805	Arg Val Arg Asp Asn Met Thr Lys Lys Met Val Thr Gln Arg Thr Ile			190	195	200	205			ggt aaa agg aag cag aga ttg aac aaa agg agt tat cta att agg gca		853	Gly Lys Arg Lys Gln Arg Leu Asn Lys Arg Ser Tyr Leu Ile Arg Ala			210	215	220	tta acc ctg aac aca atg acc aaa gat gct gag aga ggg aag cta aaa		901	Leu Thr Leu Asn Thr Met Thr Lys Asp Ala Glu Arg Gly Lys Leu Lys			225	230	235	cgg aga gca att gca acc cca ggg atg caa ata agg ggg ttt gta tac		949	Arg Arg Ala Ile Ala Thr Pro Gly Met Gln Ile Arg Gly Phe Val Tyr			240	245	250	ttt gtt gag aca cta gca agg agt ata tgt gag aaa ctt gaa caa tca		997	Phe Val Glu Thr Leu Ala Arg Ser Ile Cys Glu Lys Leu Glu Gln Ser			255	260	265	gga ttg cca gtt gga ggc aat gag aag aaa gca aag ttg gca aat gtt		1045	Gly Leu Pro Val Gly Gly Asn Glu Lys Lys Ala Lys Leu Ala Asn Val			270	275	280	285			gta agg aag atg atg acc aat tct cag gac act gaa att tct ttc acc		1093	Val Arg Lys Met Met Thr Asn Ser Gln Asp Thr Glu Ile Ser Phe Thr			290	295	300	atc act gga gat aac acc aaa tgg aac gaa aat cag aac cct cgg atg		1141	Ile Thr Gly Asp Asn Thr Lys Trp Asn Glu Asn Gln Asn Pro Arg Met			305	310	315	ttt ttg gcc atg atc aca tat ata acc aga aat cag ccc gaa tgg ttc		1189	Phe Leu Ala Met Ile Thr Tyr Ile Thr Arg Asn Gln Pro Glu Trp Phe			320	325	330	aga aat gtt cta agt att gct cca ata atg ttc tca aac aaa atg gcg		1237	Arg Asn Val Leu Ser Ile Ala Pro Ile Met Phe Ser Asn Lys Met Ala			335	340	345	aga ctg gga aag ggg tac atg ttt gag agc aag agt atg aaa att aga		1285	Arg Leu Gly Lys Gly Tyr Met Phe Glu Ser Lys Ser Met Lys Ile Arg			350	355	360	365			act caa ata cct gca gaa atg cta gca agt att gat cta aaa tat ttc		1333	Thr Gln Ile Pro Ala Glu Met Leu Ala Ser Ile Asp Leu Lys Tyr Phe			370	375	380
125																																																																																																																																																														
cg a cag acc tat gac tgg act cta aat agg aac cag cct gct gca aca		613																																																																																																																																																												
Arg Gln Thr Tyr Asp Trp Thr Leu Asn Arg Asn Gln Pro Ala Ala Thr																																																																																																																																																														
130	135	140																																																																																																																																																												
gca ttg gcc aac aca ata gaa gtg ttc aga tca aat ggc ctc acg gcc		661																																																																																																																																																												
Ala Leu Ala Asn Thr Ile Glu Val Phe Arg Ser Asn Gly Leu Thr Ala																																																																																																																																																														
145	150	155																																																																																																																																																												
aat gaa tct gga agg ctc ata gac ttc ctt aag gat gta atg gag tca		709																																																																																																																																																												
Asn Glu Ser Gly Arg Leu Ile Asp Phe Leu Lys Asp Val Met Glu Ser																																																																																																																																																														
160	165	170																																																																																																																																																												
atg aac aaa gaa gaa atg gag atc aca act cat ttt cag aga aag aga		757																																																																																																																																																												
Met Asn Lys Glu Glu Met Glu Ile Thr Thr His Phe Gln Arg Lys Arg																																																																																																																																																														
175	180	185																																																																																																																																																												
cga gtg aga gac aat atg act aag aaa atg gtg aca cag aga aca ata		805																																																																																																																																																												
Arg Val Arg Asp Asn Met Thr Lys Lys Met Val Thr Gln Arg Thr Ile																																																																																																																																																														
190	195	200	205			ggt aaa agg aag cag aga ttg aac aaa agg agt tat cta att agg gca		853	Gly Lys Arg Lys Gln Arg Leu Asn Lys Arg Ser Tyr Leu Ile Arg Ala			210	215	220	tta acc ctg aac aca atg acc aaa gat gct gag aga ggg aag cta aaa		901	Leu Thr Leu Asn Thr Met Thr Lys Asp Ala Glu Arg Gly Lys Leu Lys			225	230	235	cgg aga gca att gca acc cca ggg atg caa ata agg ggg ttt gta tac		949	Arg Arg Ala Ile Ala Thr Pro Gly Met Gln Ile Arg Gly Phe Val Tyr			240	245	250	ttt gtt gag aca cta gca agg agt ata tgt gag aaa ctt gaa caa tca		997	Phe Val Glu Thr Leu Ala Arg Ser Ile Cys Glu Lys Leu Glu Gln Ser			255	260	265	gga ttg cca gtt gga ggc aat gag aag aaa gca aag ttg gca aat gtt		1045	Gly Leu Pro Val Gly Gly Asn Glu Lys Lys Ala Lys Leu Ala Asn Val			270	275	280	285			gta agg aag atg atg acc aat tct cag gac act gaa att tct ttc acc		1093	Val Arg Lys Met Met Thr Asn Ser Gln Asp Thr Glu Ile Ser Phe Thr			290	295	300	atc act gga gat aac acc aaa tgg aac gaa aat cag aac cct cgg atg		1141	Ile Thr Gly Asp Asn Thr Lys Trp Asn Glu Asn Gln Asn Pro Arg Met			305	310	315	ttt ttg gcc atg atc aca tat ata acc aga aat cag ccc gaa tgg ttc		1189	Phe Leu Ala Met Ile Thr Tyr Ile Thr Arg Asn Gln Pro Glu Trp Phe			320	325	330	aga aat gtt cta agt att gct cca ata atg ttc tca aac aaa atg gcg		1237	Arg Asn Val Leu Ser Ile Ala Pro Ile Met Phe Ser Asn Lys Met Ala			335	340	345	aga ctg gga aag ggg tac atg ttt gag agc aag agt atg aaa att aga		1285	Arg Leu Gly Lys Gly Tyr Met Phe Glu Ser Lys Ser Met Lys Ile Arg			350	355	360	365			act caa ata cct gca gaa atg cta gca agt att gat cta aaa tat ttc		1333	Thr Gln Ile Pro Ala Glu Met Leu Ala Ser Ile Asp Leu Lys Tyr Phe			370	375	380																																																
205																																																																																																																																																														
ggt aaa agg aag cag aga ttg aac aaa agg agt tat cta att agg gca		853																																																																																																																																																												
Gly Lys Arg Lys Gln Arg Leu Asn Lys Arg Ser Tyr Leu Ile Arg Ala																																																																																																																																																														
210	215	220																																																																																																																																																												
tta acc ctg aac aca atg acc aaa gat gct gag aga ggg aag cta aaa		901																																																																																																																																																												
Leu Thr Leu Asn Thr Met Thr Lys Asp Ala Glu Arg Gly Lys Leu Lys																																																																																																																																																														
225	230	235																																																																																																																																																												
cgg aga gca att gca acc cca ggg atg caa ata agg ggg ttt gta tac		949																																																																																																																																																												
Arg Arg Ala Ile Ala Thr Pro Gly Met Gln Ile Arg Gly Phe Val Tyr																																																																																																																																																														
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ttt gtt gag aca cta gca agg agt ata tgt gag aaa ctt gaa caa tca		997																																																																																																																																																												
Phe Val Glu Thr Leu Ala Arg Ser Ile Cys Glu Lys Leu Glu Gln Ser																																																																																																																																																														
255	260	265																																																																																																																																																												
gga ttg cca gtt gga ggc aat gag aag aaa gca aag ttg gca aat gtt		1045																																																																																																																																																												
Gly Leu Pro Val Gly Gly Asn Glu Lys Lys Ala Lys Leu Ala Asn Val																																																																																																																																																														
270	275	280	285			gta agg aag atg atg acc aat tct cag gac act gaa att tct ttc acc		1093	Val Arg Lys Met Met Thr Asn Ser Gln Asp Thr Glu Ile Ser Phe Thr			290	295	300	atc act gga gat aac acc aaa tgg aac gaa aat cag aac cct cgg atg		1141	Ile Thr Gly Asp Asn Thr Lys Trp Asn Glu Asn Gln Asn Pro Arg Met			305	310	315	ttt ttg gcc atg atc aca tat ata acc aga aat cag ccc gaa tgg ttc		1189	Phe Leu Ala Met Ile Thr Tyr Ile Thr Arg Asn Gln Pro Glu Trp Phe			320	325	330	aga aat gtt cta agt att gct cca ata atg ttc tca aac aaa atg gcg		1237	Arg Asn Val Leu Ser Ile Ala Pro Ile Met Phe Ser Asn Lys Met Ala			335	340	345	aga ctg gga aag ggg tac atg ttt gag agc aag agt atg aaa att aga		1285	Arg Leu Gly Lys Gly Tyr Met Phe Glu Ser Lys Ser Met Lys Ile Arg			350	355	360	365			act caa ata cct gca gaa atg cta gca agt att gat cta aaa tat ttc		1333	Thr Gln Ile Pro Ala Glu Met Leu Ala Ser Ile Asp Leu Lys Tyr Phe			370	375	380																																																																																																
285																																																																																																																																																														
gta agg aag atg atg acc aat tct cag gac act gaa att tct ttc acc		1093																																																																																																																																																												
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Phe Leu Ala Met Ile Thr Tyr Ile Thr Arg Asn Gln Pro Glu Trp Phe																																																																																																																																																														
320	325	330																																																																																																																																																												
aga aat gtt cta agt att gct cca ata atg ttc tca aac aaa atg gcg		1237																																																																																																																																																												
Arg Asn Val Leu Ser Ile Ala Pro Ile Met Phe Ser Asn Lys Met Ala																																																																																																																																																														
335	340	345																																																																																																																																																												
aga ctg gga aag ggg tac atg ttt gag agc aag agt atg aaa att aga		1285																																																																																																																																																												
Arg Leu Gly Lys Gly Tyr Met Phe Glu Ser Lys Ser Met Lys Ile Arg																																																																																																																																																														
350	355	360	365			act caa ata cct gca gaa atg cta gca agt att gat cta aaa tat ttc		1333	Thr Gln Ile Pro Ala Glu Met Leu Ala Ser Ile Asp Leu Lys Tyr Phe			370	375	380																																																																																																																																																
365																																																																																																																																																														
act caa ata cct gca gaa atg cta gca agt att gat cta aaa tat ttc		1333																																																																																																																																																												
Thr Gln Ile Pro Ala Glu Met Leu Ala Ser Ile Asp Leu Lys Tyr Phe																																																																																																																																																														
370	375	380																																																																																																																																																												

aat gaa cca aca agg aag aaa atc gag aaa ata agg cct ctc tta ata Asn Glu Pro Thr Arg Lys Lys Ile Glu Lys Ile Arg Pro Leu Leu Ile 385 390 395	1381
gat ggg act gca tca ttg agc cct gga atg atg atg ggc atg ttc aat Asp Gly Thr Ala Ser Leu Ser Pro Gly Met Met Gly Met Phe Asn 400 405 410	1429
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aga cac acc aag act act tac tgg tgg gat ggt ctt caa tct tct gat Arg His Thr Lys Thr Tyr Trp Trp Asp Gly Leu Gln Ser Ser Asp 430 435 440 445	1525
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gaa caa atc tac cag aag tgt tgc aac cta ttc gag aaa ttc ttc cct 2293
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 Ile Glu Glu Leu Arg Arg Gln Lys
 750 755

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<213> Artificial Sequence

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Gly Thr Gly Thr Gly Tyr Thr Met Asp Thr Val Asn Arg Thr His Gln
 35 40 45

Tyr Ser Glu Arg Gly Arg Trp Thr Thr Asn Thr Glu Thr Gly Ala Pro
 50 55 60

Gln Leu Asn Pro Ile Asp Gly Pro Leu Pro Glu Asp Asn Glu Pro Ser
 65 70 75 80

Gly Tyr Ala Gln Thr Asp Cys Val Leu Glu Ala Met Ala Phe Leu Glu
 85 90 95

Glu Ser His Pro Gly Ile Phe Glu Thr Ser Cys Leu Glu Thr Met Glu
 100 105 110

Val Val Gln Gln Thr Arg Val Asp Lys Leu Thr Gln Gly Arg Gln Thr
 115 120 125

Tyr Asp Trp Thr Leu Asn Arg Asn Gln Pro Ala Ala Thr Ala Leu Ala
 130 135 140

Asn Thr Ile Glu Val Phe Arg Ser Asn Gly Leu Thr Ala Asn Glu Ser
 145 150 155 160

Gly Arg Leu Ile Asp Phe Leu Lys Asp Val Met Glu Ser Met Asn Lys
 165 170 175

Glu Glu Met Glu Ile Thr Thr His Phe Gln Arg Lys Arg Arg Val Arg
 180 185 190

Asp Asn Met Thr Lys Lys Met Val Thr Gln Arg Thr Ile Gly Lys Arg
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Lys Gln Arg Leu Asn Lys Arg Ser Tyr Leu Ile Arg Ala Leu Thr Leu
 210 215 220

Asn Thr Met Thr Lys Asp Ala Glu Arg Gly Lys Leu Lys Arg Arg Ala
 225 230 235 240

Ile Ala Thr Pro Gly Met Gln Ile Arg Gly Phe Val Tyr Phe Val Glu
 245 250 255

Thr Leu Ala Arg Ser Ile Cys Glu Lys Leu Glu Gln Ser Gly Leu Pro
 260 265 270

Val Gly Gly Asn Glu Lys Lys Ala Lys Leu Ala Asn Val Val Arg Lys
 275 280 285

Met Met Thr Asn Ser Gln Asp Thr Glu Ile Ser Phe Thr Ile Thr Gly
 290 295 300

Asp Asn Thr Lys Trp Asn Glu Asn Gln Asn Pro Arg Met Phe Leu Ala
 305 310 315 320

Met Ile Thr Tyr Ile Thr Arg Asn Gln Pro Glu Trp Phe Arg Asn Val
 325 330 335

Leu Ser Ile Ala Pro Ile Met Phe Ser Asn Lys Met Ala Arg Leu Gly
 340 345 350

Lys Gly Tyr Met Phe Glu Ser Lys Ser Met Lys Ile Arg Thr Gln Ile
 355 360 365

Pro Ala Glu Met Leu Ala Ser Ile Asp Leu Lys Tyr Phe Asn Glu Pro
 370 375 380

Thr Arg Lys Lys Ile Glu Lys Ile Arg Pro Leu Leu Ile Asp Gly Thr
 385 390 395 400
 Ala Ser Leu Ser Pro Gly Met Met Met Gly Met Phe Asn Met Leu Ser
 405 410 415
 Thr Val Leu Gly Val Ser Ile Leu Asn Leu Gly Gln Lys Arg His Thr
 420 425 430
 Lys Thr Thr Tyr Trp Trp Asp Gly Leu Gln Ser Ser Asp Asp Phe Ala
 435 440 445
 Leu Ile Val Asn Ala Pro Asn His Glu Gly Ile Gln Ala Gly Val Asn
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 Arg Phe Tyr Arg Thr Cys Lys Leu Leu Gly Ile Asn Met Ser Lys Lys
 465 470 475 480
 Lys Ser Tyr Ile Asn Arg Thr Gly Thr Phe Glu Phe Thr Ser Phe Phe
 485 490 495
 Tyr Arg Tyr Gly Phe Val Ala Asn Phe Ser Met Glu Leu Pro Ser Phe
 500 505 510
 Gly Val Ser Gly Ile Asn Glu Ser Ala Asp Met Ser Ile Gly Val Thr
 515 520 525
 Val Ile Lys Asn Asn Met Ile Asn Asn Asp Leu Gly Pro Ala Thr Ala
 530 535 540
 Gln Met Ala Leu Gln Leu Phe Ile Lys Asp Tyr Arg Tyr Thr Tyr Arg
 545 550 555 560
 Cys His Arg Gly Asp Thr Gln Ile Gln Thr Arg Arg Ser Phe Glu Ile
 565 570 575
 Lys Lys Leu Trp Glu Gln Thr His Ser Lys Ala Gly Leu Leu Val Ser
 580 585 590
 Asp Gly Gly Pro Asn Leu Tyr Asn Ile Arg Asn Leu His Ile Pro Glu
 595 600 605
 Val Cys Leu Lys Trp Glu Leu Met Asp Glu Asp Tyr Gln Gly Arg Leu
 610 615 620
 Cys Asn Pro Met Asn Pro Phe Val Ser His Lys Glu Ile Glu Ser Val
 625 630 635 640
 Asn Asn Ala Ala Val Met Pro Ala His Gly Pro Ala Lys Ser Met Glu
 645 650 655
 Tyr Asp Ala Val Ala Thr Thr His Ser Trp Ile Pro Lys Arg Asn Arg
 660 665 670
 Ser Ile Leu Asn Thr Ser Gln Arg Gly Ile Leu Glu Asp Glu Gln Met
 675 680 685
 Tyr Gln Lys Cys Cys Asn Leu Phe Glu Lys Phe Phe Pro Ser Ser Ser
 690 695 700
 Tyr Arg Arg Pro Val Gly Ile Ser Ser Met Val Glu Ala Met Val Ser
 705 710 715 720
 Arg Ala Arg Ile Asp Ala Arg Ile Asp Phe Glu Ser Gly Arg Ile Lys
 725 730 735

Lys Glu Glu Phe Ala Glu Ile Met Lys Ile Cys Ser Thr Ile Glu Glu
740 745 750

Leu Arg Arg Gln Lys
755